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OM protein - protein search, using SW model

Run on: April 12, 2005, 15:05:22 ; Search time 31.7966 seconds

(without alignments)
579,883 Million cell updates/sec

Title: US-09-905-247A-8

Perfect score: 1221
Sequence: 1 DVSPRLSGATSSSYGVFIN.....VDAQVTSNALLNPNMA 247Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/6C COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1221	100.0	267	1	US-08-378-761A-74
2	1221	100.0	267	1	US-08-485-286-74
3	1212	99.3	289	1	US-07-923-692C-4
4	1212	99.3	289	1	US-08-184-837-4
5	1212	99.3	289	2	US-08-482-920-4
6	1212	99.3	289	3	US-08-484-341-4
7	1212	99.3	289	3	US-08-483-502-4
8	1212	99.3	289	4	US-09-726-651A-4
9	1209	99.0	247	1	US-08-488-113B-6
10	1209	99.0	247	1	US-08-477-484B-6
11	1209	99.0	247	2	US-08-646-360-6
12	1209	99.0	247	3	US-08-839-765-6
13	1209	99.0	247	3	US-09-136-389-6
14	1209	99.0	247	3	US-09-610-838-6
15	1209	99.0	247	4	US-09-711-485-6
16	1137	93.1	255	1	US-07-901-707-6
17	1137	93.1	255	1	US-07-988-430-6
18	1137	93.1	255	1	US-08-425-336-6
19	1137	93.1	255	5	PCT-US92-09487-6
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22	1071	87.7	230	2	US-08-557-731-2
23	1071	87.7	436	3	US-08-902-486-15
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25	802	65.7	263	1	US-07-988-430-7
26	802	65.7	263	1	US-08-425-336-7
27	802	65.7	263	1	US-08-488-113B-7

28	802	65.7	263	1	US-08-477-484B-7	Sequence 7, App1
29	802	65.7	263	2	US-08-646-360-7	Sequence 7, App1
30	802	65.7	263	3	US-08-839-765-7	Sequence 7, App1
31	802	65.7	263	3	US-09-136-389-7	Sequence 7, App1
32	802	65.7	263	3	US-09-610-838-7	Sequence 7, App1
33	802	65.7	263	4	US-09-711-485-7	Sequence 7, App1
34	802	65.7	263	5	PCT-US92-09487-7	Sequence 7, App1
35	762	62.4	250	1	US-08-378-761A-78	Sequence 78, App1
36	762	62.4	250	1	US-08-485-286-78	Sequence 78, App1
37	724.5	59.3	248	1	US-07-901-707-5	Sequence 5, App1
38	724.5	59.3	248	1	US-07-988-430-5	Sequence 5, App1
39	724.5	59.3	248	1	US-08-425-336-5	Sequence 5, App1
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41	724.5	59.3	248	1	US-08-485-286-75	Sequence 75, App1
42	724.5	59.3	248	1	US-08-488-113B-5	Sequence 5, App1
43	724.5	59.3	248	1	US-08-477-484B-5	Sequence 5, App1
44	724.5	59.3	248	2	US-08-646-360-5	Sequence 5, App1
45	724.5	59.3	248	3	US-08-839-765-5	Sequence 5, App1

ALIGNMENTS

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RESULT 1
US-08-378-761A-74
; Sequence 74, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 382728
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-761A-74

Query Match      100.0%; Score 1221; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.6e-119; Indels 0; Gaps 0;
Matches 247; Conservative 0; Mismatches 0;

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DB 2 DVSPRLSGATSSSYGVFINLRKALPNERKLYDIPLRSSLPQSORVALIHTNVADEFT 61
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Db 62 SVAIDVTNYIMGYRAGDTSYFNEASATEAAKYFKDAMRKVTLPSYGNVERLQTAAGK 121
| | | | |
QY 121 IRENIPGLPALDSATITLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTKFL 180
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Db 122 IRENIPGLPALDSATITLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTKFL 181
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QY 181 PSLAIIISLNSWSALSQIOIASTNNGOFESPVLINQNRVTITNVDAGVTSNIALL 240
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Db 182 PSLAIIISLNSWSALSQIOIASTNNGOFESPVLINQNRVTITNVDAGVTSNIALL 241
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QY 241 LNRNNMA 247
| | | | |
Db 242 LNRNNMA 248

RESULT 2
US-08-485-286-74
; Sequence 74, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-286-74

Query Match 100.0%; Score 1221; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 2,6e-119;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPSSQRYALIHILTNVADERT 60
| | | | |
Db 2 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPSSQRYALIHILTNVADERT 61
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QY 61 SVAIDVTNYIMGYRAGDTSYFNEASATEAAKYFKDAMRKVTLPSYGNVERLQTAAGK 120
| | | | |
Db 62 SVAIDVTNYIMGYRAGDTSYFNEASATEAAKYFKDAMRKVTLPSYGNVERLQTAAGK 121
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QY 121 IRENIPGLPALDSATITLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTKFL 180
| | | | |
Db 122 IRENIPGLPALDSATITLFFYNNANSASALMWLIQSTSEARRYFIEQOIGKRVDTKFL 181
| | | | |
QY 181 PSLAIIISLNSWSALSQIOIASTNNGOFESPVLINQNRVTITNVDAGVTSNIALL 240
| | | | |
Db 182 PSLAIIISLNSWSALSQIOIASTNNGOFESPVLINQNRVTITNVDAGVTSNIALL 241
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QY 241 LNRNNMA 247
| | | | |
Db 242 LNRNNMA 248

RESULT 3
US-07-923-692C-4
; Sequence 4, Application US/07923692C
; Patent No. 5316931
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William O.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grillo, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Perry Building
; CITY: San Francisco
; STATE: CAL
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/923,692C
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,244
; FILING DATE: 22-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 641,617
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 310,881
; FILING DATE: 17-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,766
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,771
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 347,637
; FILING DATE: 05-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 363,138
; FILING DATE: 08-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 219,279
; FILING DATE: 15-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 28,957

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; REFERENCE/DOCKET NUMBER: BIOC-20121
; REFERENCE/DOCKET NUMBER: USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-433-4150
; TELEFAX: 415-433-8716
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-07-923-692C-4

Query Match          99.3%; Score 1212; DB 1; Length 289;
Best Local Similarity 99.2%; Pred. No. 2.5e-118;
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 84 SVAIDVTNVIYIMGRAGDTSYFENEASATEAKYVFCDAMRKVTLLPYSGNYERLQTPAGK 143
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DB 144 IRENIPILGIPALDSATITLFFYNNANSASALMWLIQSTSEARXYKIEQOIGKRVDKTFL 203
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DB 204 PSIAITSLNSWSALSKQIQIASTNNQGFETPVVLIQAQORVTITNVDAVVTSTNIAL 263
QY 241 LNRNNMA 247
DB 264 LNRNNMA 270

RESULT 4
US-08-184-237-4
; Sequence 4, Application US/08184237
; Patent No. 5589367
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William O.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grillo, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CAL
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,237
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 923,692
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,244
; FILING DATE: 22-OCT-1990

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 641,617
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 310,881
; FILING DATE: 17-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,766
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,771
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 347,637
; FILING DATE: 05-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 363,138
; FILING DATE: 08-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 219,279
; FILING DATE: 15-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: BIOC-20121 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-433-4150
; TELEFAX: 415-433-8716
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 289 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-184-237-4

Query Match          99.3%; Score 1212; DB 1; Length 289;
Best Local Similarity 99.2%; Pred. No. 2.5e-118;
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRRKALPNERKLYDIPILRRSLPGSORYALHITNVADETI 60
DB 24 DVSFRLSGATSSSYGVFISNLRRKALPNERKLYDIPILRRSLPGSORYALHITNVADETI 83
QY 61 SVAIDVTNVIYIMGRAGDTSYFENEASATEAKYVFCDAMRKVTLLPYSGNYERLQTPAGK 120
DB 84 SVAIDVTNVIYIMGRAGDTSYFENEASATEAKYVFCDAMRKVTLLPYSGNYERLQTPAGK 143
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DB 144 IRENIPILGIPALDSATITLFFYNNANSASALMWLIQSTSEARXYKIEQOIGKRVDKTFL 203
QY 181 PSIAITSLNSWSALSKQIQIASTNNQGFESPVVLINAQORVTITNVDAVVTSTNIAL 240
DB 204 PSIAITSLNSWSALSKQIQIASTNNQGFETPVVLIQAQORVTITNVDAVVTSTNIAL 263
QY 241 LNRNNMA 247
DB 264 LNRNNMA 270

RESULT 5
US-08-482-920-4
; Sequence 4, Application US/08482920
; Patent No. 5866785
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William O.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grillo, Laurence K.

```

TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penmie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,920
 FILING DATE: 07-JUNE-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 184,237
 FILING DATE: 19-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 600,244
 FILING DATE: 22-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 641,617
 FILING DATE: 16-JAN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 310,881
 FILING DATE: 17-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,766
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,771
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 347,637
 FILING DATE: 05-MAY-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 363,138
 FILING DATE: 08-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 219,279
 FILING DATE: 15-JUL-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 8129-112
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-3660
 TELEFAX: 415-854-3694
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 289 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-482-920-4

Query Match	99.3%	Score 1212	DB 2	Length 289
Best Local Similarity	99.2%	Pred. No. 2.5e-118		
Matches 245	Conservative 1	Mismatches 1	Indels 0	Gaps 0
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Db	24	DVSFRLSGATSSSYGVIFSNLRKALPNEKKLYDIPLRSSLPGSORVALIHLTVADETI	83	
QY	61	SVAIDVTNYINGYRAGDTSYFFPNEASATEAKYVFKDAMRKVTLPSGNYERLQTAGK	120	
Db	84	SVAIDVTNYINGYRAGDTSYFFPNEASATEAKYVFKDAMRKVTLPSGNYERLQTAGK	143	
QY	121	IRRNIPGLGPALDSATTLTFYNNANSASALMWLIQSTSEARKYFTEQIGKRVDTFL	180	
Db	144	IRRNIPGLGPALDSATTLTFYNNANSASALMWLIQSTSEARKYFTEQIGKRVDTFL	203	

Qy	181	PSLAIISLENSWSALSKQIQIASTNNGQFESPVLINQORVITIVNDAQVTSINALL	240
Db	204	PSLAIISLENSWSALSKQIQIASTNNGQFEPVVLINQORVITIVNDAQVTSINALL	263
Qy	241	LNENNNMA	247
Db	264	LNENNNMA	270

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1      RESULT 6
2      US-08-484-341-4
3      ; Sequence 4, Application US/08/484341
4      ; GENERAL INFORMATION:
5      ;   APPLICANT: Donson, Jon
6      ;   Dawson, William O.
7      ;   Grantham, George L.
8      ;   Turpen, Thomas H.
9      ;   Turpen, Ann Myers
10     ;   Garger, Stephen U.
11     ;   Gfill, Laurence K.
12     ;
13     ; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
14     ;
15     ; NUMBER OF SEQUENCES: 11
16     ;
17     ; CORRESPONDENCE ADDRESS:
18     ;   ADDRESSER: Limbach & Limbach
19     ;   STREET: 2001 Ferry Building
20     ;   CITY: San Francisco
21     ;   STATE: CAL
22     ;   ZIP: 94111
23     ;
24     ; COMPUTER READABLE FORM:
25     ;   MEDIUM TYPE: Floppy disk
26     ;   COMPUTER: IBM PC compatible
27     ;   OPERATING SYSTEM: PC-DOS/MS-DOS
28     ;   SOFTWARE: Patent in Release #1.0, Version #1.25
29     ;
30     ; CURRENT APPLICATION DATA:
31     ;   APPLICATION NUMBER: US/08/484,341
32     ;   FILING DATE: 07-Jun-1995
33     ;   CLASSIFICATION: <Unknown>
34     ;
35     ; PRIOR APPLICATION DATA:
36     ;   APPLICATION NUMBER: 08/184,237
37     ;   FILING DATE: <Unknown>
38     ;   APPLICATION NUMBER: US 600,244
39     ;   FILING DATE: 22-OCT-1990
40     ;   APPLICATION NUMBER: US 641,617
41     ;   FILING DATE: 16-JAN-1991
42     ;   APPLICATION NUMBER: US 310,881
43     ;   FILING DATE: 17-FEB-1989
44     ;   APPLICATION NUMBER: US 160,766
45     ;   FILING DATE: 26-FEB-1988
46     ;   APPLICATION NUMBER: US 160,771
47     ;   FILING DATE: 26-FEB-1988
48     ;   APPLICATION NUMBER: US 347,637
49     ;   FILING DATE: 03-MAY-1989
50     ;   APPLICATION NUMBER: US 363,138
51     ;   FILING DATE: 08-JUN-1989
52     ;   APPLICATION NUMBER: US 219,279
53     ;   FILING DATE: 15-JUL-1988
54     ;
55     ; ATTORNEY/AGENT INFORMATION:
56     ;   NAME: Halluin, Albert P.
57     ;   REGISTRATION NUMBER: 28,957
58     ;   REFERENCE/DOCKET NUMBER: BIOG-20121 USA
59     ;
60     ; TELECOMMUNICATION INFORMATION:
61     ;   TELEPHONE: 415-433-4150
62     ;   TELEFAX: 415-433-8716
63     ;
64     ; INFORMATION FOR SEQ ID NO: 4:
65     ;   SEQUENCE CHARACTERISTICS:
66     ;     LENGTH: 289 amino acids
67     ;     TYPE: amino acid
68     ;     TOPOLOGY: linear
69     ;
70     ; MOLECULE TYPE: protein
71     ;
72     ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
73     ;
74     ; US-08-484-341-4

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Query Match 99.3%; Score 1212; DB 3; Length 289;
 Best Local Similarity 99.2%; Pred. No. 2,5e-118;
 Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 60
 DB 24 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 83
 QY 61 SVAIDVTNVIYINGRAGDTSYFNEASATEAKYVFDAMRKVTLPYSGYERLQTPAGK 120
 DB 84 SVAIDVTNVIYINGRAGDTSYFNEASATEAKYVFDAMRKVTLPYSGYERLQTPAGK 143
 QY 121 IRENIPGLPALDSATITLTFYNNANSAALMWLIQSTSEARXKFTIEQIGKRVKDTFL 180
 DB 144 IRENIPGLPALDSATITLTFYNNANSAALMWLIQSTSEARXKFTIEQIGKRVKDTFL 203
 QY 181 PSIAIISLNSWSALSQKQIQAISTNNGQFESSPVVLIINAQORVTITNVDAVVTSNIAL 240
 DB 204 PSIAIISLNSWSALSQKQIQAISTNNGQFETPVVLIINAQORVTITNVDAVVTSNIAL 263
 QY 241 LNRRNMA 247
 DB 264 LNRRNMA 270

RESULT 7
 US-08-483-502-4
 Sequence 4, Application US/08483502
 Patent No. 6284492

GENERAL INFORMATION:

APPLICANT: Donson, Jon
 APPLICANT: Dawson, William O.
 APPLICANT: Grantham, George L.
 APPLICANT: Turpen, Thomas H.
 APPLICANT: Turpen, Ann M.
 APPLICANT: Garger, Stephen J.
 APPLICANT: Grill, Laurence K.
 TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 STREET: 1201 New York Avenue N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,502
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/739,143
 FILING DATE:
 APPLICATION NUMBER: US 600,244
 FILING DATE: 22-OCT-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 641,617
 FILING DATE: 16-JAN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 310,881
 FILING DATE: 17-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,766
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 160,771
 FILING DATE: 26-FEB-1988
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 347,637
 FILING DATE: 05-MAY-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 363,138
 FILING DATE: 08-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 219,279
 FILING DATE: 15-JUL-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Ihnen, Jeffrey L.
 REGISTRATION NUMBER: 28,957
 REFERENCE/DOCKET NUMBER: 18604-090574
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-962-4810
 TELEFAX: 202-962-8300
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 289 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-483-502-4

Query Match 99.3%; Score 1212; DB 3; Length 289;
 Best Local Similarity 99.2%; Pred. No. 2,5e-118;
 Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 60
 DB 24 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADETI 83
 QY 61 SVAIDVTNVIYINGRAGDTSYFNEASATEAKYVFDAMRKVTLPYSGYERLQTPAGK 120
 DB 84 SVAIDVTNVIYINGRAGDTSYFNEASATEAKYVFDAMRKVTLPYSGYERLQTPAGK 143
 QY 121 IRENIPGLPALDSATITLTFYNNANSAALMWLIQSTSEARXKFTIEQIGKRVKDTFL 180
 DB 144 IRENIPGLPALDSATITLTFYNNANSAALMWLIQSTSEARXKFTIEQIGKRVKDTFL 203
 QY 181 PSIAIISLNSWSALSQKQIQAISTNNGQFESSPVVLIINAQORVTITNVDAVVTSNIAL 240
 DB 204 PSIAIISLNSWSALSQKQIQAISTNNGQFETPVVLIINAQORVTITNVDAVVTSNIAL 263
 QY 241 LNRRNMA 247
 DB 264 LNRRNMA 270

RESULT 8
 US-09-726-651A-4
 Sequence 4, Application US/09726651A
 Patent No. 6448046

GENERAL INFORMATION:

APPLICANT: Donson, Jon
 APPLICANT: Dawson, William O.
 APPLICANT: Grantham, George L.
 APPLICANT: Turpen, Thomas H.
 APPLICANT: Turpen, Ann M.
 APPLICANT: Garger, Stephen J.
 APPLICANT: Grill, Laurence K.
 TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
 FILE REFERENCE: 008010023CNU001
 CURRENT APPLICATION NUMBER: US/09/726,651A
 CURRENT FILING DATE: 2002-05-02
 PRIOR APPLICATION NUMBER: 08/483,502
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/184,237
 PRIOR FILING DATE: 1994-01-19
 PRIOR APPLICATION NUMBER: 07/923,692
 PRIOR FILING DATE: 1992-07-31
 PRIOR APPLICATION NUMBER: 07/600,244
 PRIOR FILING DATE: 1990-10-22
 PRIOR APPLICATION NUMBER: 07/641,617

;; PRIOR FILING DATE: 1991-01-16
;; PRIOR APPLICATION NUMBER: 07/737,899
;; PRIOR FILING DATE: 1991-07-26
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: FaastSeq for Windows Version 4.0
;; SEQ ID NO: 4
;; LENGTH: 289
;; TYPE: PRT
;; ORGANISM: Chinese Cucumber alpha-crucosanthin
US-09-726-651A-4

Query Match 99.3%; Score 1212; DB 4; Length 289;
Best Local Similarity 99.2%; Pred. No. 2,5e-118;
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
DB 24 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 83
QY 61 SVAIDVTNYIIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPSGNYERLQTAAGK 120
DB 84 SVAIDVTNYIIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPSGNYERLQTAAGK 143
QY 121 IRENIPILGLPALDSATITLFFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDKTFL 180
DB 144 IRENIPILGLPALDSATITLFFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDKTFL 203
QY 181 PSIAIISLNSWSALSKQIQIASTNNGOFESPVLINQONRVITTNVAGVTSNIALL 240
DB 204 PSIAIISLNSWSALSKQIQIASTNNGOFESPVLINQONRVITTNVAGVTSNIALL 263
QY 241 LNRNNMA 247
DB 264 LNRNNMA 270

RESULT 9

US-08-488-113B-6
; Sequence 6, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroli, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 247 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULAR TYPE: protein
US-08-488-113B-6

Query Match 99.0%; Score 1209; DB 1; Length 247;
Best Local Similarity 99.2%; Pred. No. 4.1e-118;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
DB 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
QY 61 SVAIDVTNYIIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPSGNYERLQTAAGK 120
DB 61 SVAIDVTNYIIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPSGNYERLQTAAGK 120
QY 121 IRENIPILGLPALDSATITLFFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDKTFL 180
DB 121 IRENIPILGLPALDSATITLFFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDKTFL 180
QY 181 PSIAIISLNSWSALSKQIQIASTNNGOFESPVLINQONRVITTNVAGVTSNIALL 240
DB 181 PSIAIISLNSWSALSKQIQIASTNNGOFESPVLINQONRVITTNVAGVTSNIALL 240
QY 241 LNRNNMA 247
DB 241 LNRNNMA 247

RESULT 10

US-08-477-484B-6
; Sequence 6, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroli, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-6

Query Match 99.0%; Score 1209; DB 1; Length 247;
Best Local Similarity 99.2%; Pred. No. 4.1e-118;

Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
QY 61 SVAIDVTNVIYIMGRAGDTSYFPNEASATEBAKYVFKDAMRKVTLTPYSGYERLQTPACK 120
DB 61 SVAIDVTNVIYIMGRAGDTSYFPNEASATEBAKYVFKDAMRKVTLTPYSGYERLQTPACK 120
QY 121 IRENIPGLPALDSATITLTFYNNANGASALMWLIQSTSEAAKYKIEQOIGRVKXFL 180
DB 121 IRENIPGLPALDSATITLTFYNNANGASALMWLIQSTSEAAKYKIEQOIGRVKXFL 180
QY 181 PSIAIISLENSWSALSQKQIQAISTNNGQFESPVLINAQORVTITNVDAVGTSTNIAL 240
DB 181 PSIAIISLENSWSALSQKQIQAISTNNGQFESPVLINAQORVTITNVDAVGTSTNIAL 240
QY 241 LNRNMA 247
DB 241 LNRNMA 247

RESULT 11

US-08-646-360-6
Sequence 6, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-6

Query Match 99.0%; Score 1209; DB 2; Length 247;
Best Local Similarity 99.2%; Pred. No. 4.1e-118;

Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
QY 61 SVAIDVTNVIYIMGRAGDTSYFPNEASATEBAKYVFKDAMRKVTLTPYSGYERLQTPACK 120
DB 61 SVAIDVTNVIYIMGRAGDTSYFPNEASATEBAKYVFKDAMRKVTLTPYSGYERLQTPACK 120
QY 121 IRENIPGLPALDSATITLTFYNNANGASALMWLIQSTSEAAKYKIEQOIGRVKXFL 180
DB 121 IRENIPGLPALDSATITLTFYNNANGASALMWLIQSTSEAAKYKIEQOIGRVKXFL 180
QY 181 PSIAIISLENSWSALSQKQIQAISTNNGQFESPVLINAQORVTITNVDAVGTSTNIAL 240
DB 181 PSIAIISLENSWSALSQKQIQAISTNNGQFESPVLINAQORVTITNVDAVGTSTNIAL 240
QY 241 LNRNMA 247
DB 241 LNRNMA 247

RESULT 12

US-08-839-765-6
Sequence 6, Application US/08839765
Patent No. 614631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 110220809/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-6

Query Match 99.0%; Score 1209; DB 3; Length 247;
Best Local Similarity 99.2%; Pred. No. 4.1e-118;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
QY 61 SVVAVDTNYYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120
DB 61 SVVAVDTNYYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120
QY 121 IRENIPLGIPALDSATITLFPYNNANSAASALMWLLOSTSEAAKYRTEEOIGRVYDKFTL 180
DB 121 IRENIPLGIPALDSATITLFPYNNANSAASALMWLLOSTSEAAKYRTEEOIGRVYDKFTL 180
QY 181 PSLAIIISLENSWSALSQIOIASTNNGQFESPVLINAOQRVTITNVAGVTSNIALI 240
DB 181 PSLAIIISLENSWSALSQIOIASTNNGQFESPVLINAOQRVTITNVAGVTSNIALI 240
QY 241 ILRNNMA 247
DB 241 ILRNNMA 247

DB 241 ILRNNMA 247

RESULT 13
US-09-136-389-6
Sequence 6, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-6

Query Match 99.0%; Score 1209; DB 3; Length 247;
Best Local Similarity 99.2%; Pred. No. 4.1e-118;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
QY 61 SVVAVDTNYYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120
DB 61 SVVAVDTNYYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120

Db 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKDMARKVTLPYSGNYERLQTAAGK 120
QY 121 IRENIFLG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGRVDTFL 180
Db 121 IRENIFLG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGRVDTFL 180
QY 181 PSIAITISLNSWSALSQKQIQIASTNNGQFESPVLINAOQRVTITNVDAVVTSNIAL 240
Db 181 PSIAITISLNSWSALSQKQIQIASTNNGQFESPVLINAOQRVTITNVDAVVTSNIAL 240
QY 241 LNRNNMA 247
Db 241 LNRNNMA 247
RESULT 14
US-09-610-838-6
Sequence 6, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70, P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-6
Query Match 99.0%; Score 1209; DB 3; Length 247;
Best Local Similarity 99.2%; Pred. No. 4,1e-118;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 DVSFRLSGATSSSYGYFISNLRKALPNERKLYDIPILRSLSLPGSQRYALIHLTNVADETI 60
Db 1 DVSFRLSGATSSSYGYFISNLRKALPNERKLYDIPILRSLSLPGSQRYALIHLTNVADETI 60
QY 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKDMARKVTLPYSGNYERLQTAAGK 120
Db 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKDMARKVTLPYSGNYERLQTAAGK 120
QY 121 IRENIFLG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGRVDTFL 180
Db 121 IRENIFLG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFEQOIGRVDTFL 180
QY 181 PSIAITISLNSWSALSQKQIQIASTNNGQFESPVLINAOQRVTITNVDAVVTSNIAL 240
Db 181 PSIAITISLNSWSALSQKQIQIASTNNGQFESPVLINAOQRVTITNVDAVVTSNIAL 240
QY 241 LNRNNMA 247
Db 241 LNRNNMA 247
RESULT 15
US-09-711-485-6
Sequence 6, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-711-485-6

Query Match 99.0%; Score 1209; DB 4; Length 247;
Best local Similarity 99.2%; Pred. No. 4,1e-118;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPLLRSSLPQSQRVALIHLTNVADETI	60
Db	1	DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPLLRSSLPQSQRVALIHLTNVADETI	60
QY	61	SVAIIDVTNYIMGYRAGDTSYFPNEASATEAAKYVEKDMARKVTLPYSGNYERLQTAAGK	120
Db	61	SVAIIDVTNYIMGYRAGDTSYFPNEASATEAAKYVEKDMARKVTLPYSGNYERLQTAAGK	120
QY	121	IRENIPLGIPALDSAITTLFPYNNANSASALMWLIOSTSEAAKYKFIEOQIGKVDKFTL	180
Db	121	IRENIPLGIPALDSAITTLFPYNNANSASALMWLIOSTSEAAKYKFIEOQIGKVDKFTL	180
QY	181	PSLAISLSENSWALSKEQIQIASTNNGQEPSPVVLINAQNRVTITNVDAGVVTSNIALLL	240
Db	181	PSLAISLSENSWALSKEQIQIASTNNGQEPSPVVLINAQNRVTITNVDAGVVTSNIALLL	240
QY	241	LNRRNNMA 247	
Db	241	LNRRNNMA 247	

Search completed: April 12, 2005, 15:16:15
Job time : 32.7966 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2005, 14:53:56 ; Search time 111.519 Seconds

(without alignments)
856.626 Million cell updates/sec

Title: US-09-905-247A-8

Perfect score: 1221
Sequence: 1 DVSPRLSGATSSSYGVFISN.....VDAGVTSNIALLNANMA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1221	100.0	247	3	AAV69048
2	1221	100.0	248	2	AAV69048
3	1221	100.0	248	2	AAV69048
4	1221	100.0	248	2	AAV69048
5	1221	100.0	248	2	AAV69048
6	1221	100.0	248	2	AAV69048
7	1221	100.0	248	2	AAV69048
8	1221	100.0	248	2	AAV69048
9	1221	100.0	248	2	AAV69048
10	1221	100.0	248	2	AAV69048
11	1221	100.0	248	2	AAV69048
12	1221	100.0	248	2	AAV69048
13	1221	100.0	248	2	AAV69048
14	1221	100.0	248	2	AAV69048
15	1221	100.0	248	2	AAV69048
16	1221	100.0	248	2	AAV69048
17	1221	100.0	248	2	AAV69048
18	1221	100.0	248	2	AAV69048
19	1221	100.0	248	2	AAV69048
20	1221	100.0	248	2	AAV69048
21	1221	100.0	248	2	AAV69048
22	1221	100.0	248	2	AAV69048
23	1221	100.0	248	2	AAV69048
24	1221	100.0	248	2	AAV69048
25	1221	100.0	248	2	AAV69048

26	1137	93.1	255	2	AAV37295	AAV37295 Plant typ
27	1137	93.1	255	2	AAV37295	AAV37295 Plant typ
28	1071	87.7	247	3	AAV69043	AAV69043 Amino aci
29	1071	87.7	248	4	AAV68824	AAV68824 Residues
30	1071	87.7	267	8	AAV01299	AAV01299 Wild type
31	1071	87.7	267	8	AAV05683	AAV05683 Bryonia d
32	1071	87.7	290	2	AAV92481	AAV92481 Bryodin 1
33	1071	87.7	496	4	AAV36828	AAV36828 B11-G28-5
34	1044	85.5	267	3	AAV01300	AAV01300 Altered b
35	886	72.6	267	8	AAV05689	AAV05689 Bryonia d
36	802	65.7	263	2	AAV63908	AAV63908 Type I ri
37	802	65.7	263	2	AAV74182	AAV74182 Type I ri
38	795	65.1	263	2	AAV37296	AAV37296 Plant typ
39	762	62.4	250	2	AAV21707	AAV21707 Memordin
40	762	62.4	250	2	AAV25144	AAV25144 Memordin
41	754	61.8	277	2	AAV29909	AAV29909 Prod. of
42	740	60.6	272	2	AAV07522	AAV07522 Alpha-Tri
43	740	60.6	272	2	AAV25577	AAV25577 Ribosome
44	728.5	59.7	278	2	AAV29910	AAV29910 Prod. of
45	728.5	59.7	280	2	AAV07521	AAV07521 Alpha-Tri

ALIGNMENTS

RESULT 1	AAV69048	standard; protein; 247 AA.
ID	AAV69048	
AC	AAV69048	
DT	06-AUG-2003	(revised)
DT	30-MAY-2000	(first entry)
DE	Amino acid sequence of exemplary cell toxin trichosanthin.	
XX	Chemokine receptor; ligand; inflammatory response; immune effector cell;	
XX	secondary tissue damage; central nervous system injury; trichosanthin;	
XX	CNS inflammatory disease; neurodegenerative disorder; heart disease;	
XX	inflammatory eye disease; inflammatory bowel disease; PCR primer;	
XX	inflammatory joint disease; inflammatory kidney; renal disease;	
XX	inflammatory lung disease; inflammatory nasal disease; thyroiditis;	
XX	inflammatory thyroid disease; cytokine-regulated cancer; ss.	
OS	Trichosanthes kirilowii.	
PN	WO200004926-A2.	
XX	03-FEB-2000.	
PD	21-JUL-1999; 99WO-CA000659.	
PF	22-JUL-1998; 98US-00120523.	
PR	(OSPR-) OSPREY PHARM LTD.	
PA	McDonald JR, Coggin PJ;	
XX	WPI; 2000-182542/16.	
PI	A new therapeutic agent comprising a conjugate for treating secondary	
PT	tissue damage and other disease conditions like Alzheimer's disease,	
PT	stroke, Parkinson's disease and atherosclerosis.	
XX	Disclosure; Page 67; 204pp; English.	
XX	The present sequence represents an exemplary cell toxin, which can be	
XX	incorporated into the conjugates of the invention. The specification	
XX	describes a conjugate, comprising a targeted agent and a chemokine	
XX	receptor ligand. The conjugate binds to a chemokine receptor resulting in	
XX	internalisation of the targeted agent in cells bearing the receptor. The	
XX	conjugates are used for formulating a medicament or for treating	
XX	disorders associated with inflammatory responses resulting from	

CC activation, proliferation and migration of immune effector cells. The
CC disorders or disease states comprise secondary tissue damage such as
CC central nervous system (CNS) injury, CNS inflammatory diseases,
CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal
CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-
CC regulated cancers. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 1221; DB 3; Length 247;
Best Local Similarity 100.0%; Pred. No. 9e-111;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFPLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNYADETI 60
DB 1 DVSFPLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNYADETI 60

QY 61 SVAIDVTNVIYMGVAGDTSYFENASATEAKVYFKDAMRKVTLPYSGNYERLQTAAGK 120
DB 61 SVAIDVTNVIYMGVAGDTSYFENASATEAKVYFKDAMRKVTLPYSGNYERLQTAAGK 120

QY 121 IRENIPLGIPALDSAITTLFYNNANSASALMWLIQSTSEARVYFIEQIQGRVDKTFPL 180
DB 121 IRENIPLGIPALDSAITTLFYNNANSASALMWLIQSTSEARVYFIEQIQGRVDKTFPL 180

QY 181 PSLAIISLSENSWALSLSKQIQIASTNNGQFESPVPVLINQONRVITTNVDAVVTSNIALL 240
DB 181 PSLAIISLSENSWALSLSKQIQIASTNNGQFESPVPVLINQONRVITTNVDAVVTSNIALL 240

QY 241 LNRNNMA 247
DB 241 LNRNNMA 247

RESULT 2
AAR07518
ID AAR07518 standard; protein; 248 AA.
XX
AC AAR07518;
XX
DT 06-FEB-1991 (first entry)
XX
DE Synthetic alpha-trichosanthin.
XX
KW trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.
XX
OS Trichosanthes kirilowii.
XX
PN WO9012097-A.
XX
PD 18-OCT-1990.
XX
PF 04-APR-1989; 89US-00333184.
XX
PR 04-APR-1989; 89US-00333184.
XX
PA (GENE-) GENELABS INC.
XX
PI Platek M, Chow T, Fry K;
XX
DR WPI: 1990-334847/44.
XX
DR N-PSDB; AAQ06346.
XX
PT Recombinant tri:chosanthin protein - with selective inhibitory effect on
XX viral expression in HIV infected T-cells or monocyte-macrophase.
XX
PS Example; Fig 11; 102pp; English.
XX
CC Encoded by a synthetic gene containing unique restriction sites spaced 20
CC to 90 bp apart. Introduction of mutations is facilitated by cassette
CC replacement. The effect of mutations on inhibitory action can be

CC investigated. For example, a double mutant containing the amino acid
CC substitutions Glu(160) to Asp and Arg(163) to Lys was found to be almost
CC 3 logs less active at inhibiting in vitro translation in rabbit
CC reticulocyte lysate. See also AAQ06343-5 and AAQ06347-Q06351
XX
SQ Sequence 248 AA;

Query Match 100.0%; Score 1221; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 9.1e-111;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFPLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNYADETI 60
DB 2 DVSFPLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNYADETI 61

QY 61 SVAIDVTNVIYMGVAGDTSYFENASATEAKVYFKDAMRKVTLPYSGNYERLQTAAGK 120
DB 62 SVAIDVTNVIYMGVAGDTSYFENASATEAKVYFKDAMRKVTLPYSGNYERLQTAAGK 121

QY 121 IRENIPLGIPALDSAITTLFYNNANSASALMWLIQSTSEARVYFIEQIQGRVDKTFPL 180
DB 122 IRENIPLGIPALDSAITTLFYNNANSASALMWLIQSTSEARVYFIEQIQGRVDKTFPL 181

QY 181 PSLAIISLSENSWALSLSKQIQIASTNNGQFESPVPVLINQONRVITTNVDAVVTSNIALL 240
DB 182 PSLAIISLSENSWALSLSKQIQIASTNNGQFESPVPVLINQONRVITTNVDAVVTSNIALL 241

QY 241 LNRNNMA 247
DB 242 LNRNNMA 248

RESULT 3
AAR25573
ID AAR25573 standard; protein; 248 AA.
XX
AC AAR25573;
XX
DT 25-MAR-2003 (revised)
XX
DT 13-JAN-1993 (first entry)
XX
DE Mature alpha-Trichosanthin.
XX
KW TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient;
XX ribosome inactivating protein; RIP; HIV-infected human T cells;
XX human immunodeficiency virus; Trichosanthes kirilowii; ss.
XX
OS Synthetic.
XX
PN US5128460-A.
XX
PD 07-JUL-1992.
XX
PF 04-APR-1990; 90US-00504775.
XX
PR 04-APR-1989; 89US-00333184.
XX
PR 07-SEP-1989; 89US-00404326.
XX
PA (GENE-) GENELABS INC.
XX
PI Platek M, Chow TP, Fry K;
XX
DR WPI: 1992-249485/30.
XX
DR N-PSDB; AAQ25573.
XX
PT Nucleic acid encoding trichosanthin protein - which can be used to
XX inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV
XX expression.
XX
PS Example 6; Fig 11; 53pp; English.
XX
CC A synthetic alpha-trichosanthin gene was constructed to facilitate
CC mutational analysis of alpha-TCS in experiments to investigate structure-

CC function relationships. The synthetic gene contains unique restriction
 CC sites spaced 20-90bp apart. The translation product of the synthetic gene
 CC corresponds to the mature alpha-TCS. Variants of the protein can be
 CC generated by mutagenesis of the synthetic gene. The variants can then be
 CC screened for changes in ribosome inhibitory and/or HIV-1 inhibitory
 CC activities. See AAQ26499-Q26505. (Updated on 25-MAR-2003 to correct PF
 CC field.) (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 248 AA;

Query Match 100.0%; Score 1221; DB 2; Length 248;

Best Local Similarity 100.0%; Pred. No. 9, 1e-111; Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSGYGFISNLKRALPNERKLYDIPILRSSLPGSQRYALHILTNVADDT 60
 DB 2 DVSFRLSGATSSGYGFISNLKRALPNERKLYDIPILRSSLPGSQRYALHILTNVADDT 61
 QY 61 SVADVTNYIMGYRAGDTSYFFNEASATEAKYVFDARKKTYLPYSGYERLQTPAGK 120
 DB 62 SVADVTNYIMGYRAGDTSYFFNEASATEAKYVFDARKKTYLPYSGYERLQTPAGK 121
 QY 121 IRENIPILGLPALDSATTTLPYNNANSASALMWLIQSTSEARARYKFTIEQIGKRVKTF 180
 DB 122 IRENIPILGLPALDSATTTLPYNNANSASALMWLIQSTSEARARYKFTIEQIGKRVKTF 181
 QY 181 PSIAITISLENSWSALSKQIQIASTNNQGFESPVLINAQNRVTITNVDAVVTSNIAL 240
 DB 182 PSIAITISLENSWSALSKQIQIASTNNQGFESPVLINAQNRVTITNVDAVVTSNIAL 241
 QY 241 LNRRNMA 247
 DB 242 LNRRNMA 248

RESULT 4

AAW21703
 ID AAW21703 standard; protein; 267 AA.

AC AAW21703;
 DT 25-MAR-2003 (revised)
 DT 26-SEP-1997 (first entry)

XX Trichosanthin.

XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat;
 KW ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.

XX Trichosanthes kirilowii.

XX Key Location/Qualifiers

FT Region 139..149
 FT /note="Position of possible insertion of internal
 FT peptide linker sequence"

XX US5635384-A.

XX 03-JUN-1997.

XX 26-JAN-1995; 95US-00378761.

XX 11-JUN-1990; 90US-00535636.

XX 09-DEC-1992; 92US-00987927.

XX (DOWC) DOWELANCO.

XX Hey TD, Morgan AER, Walsh TA;

XX WPI; 1997-309831/28.

PT Inactive precursor of maize ribosome-inactivating protein - also chimeric
 PT ribosome-inactivating protein precursors containing internal linker
 PT sequences.

XX Claim 2; Col 115-118; 121p; English.

CC The sequences given in AAW21698-710 represent Ribosome Inactivating
 CC Proteins (RIPs), which may be used in the construction of the proRIP of
 CC the invention. The proRIP has a selectively removable, internal peptide
 CC linker. The precursor sequence is incapable of inactivating eukaryotic
 CC ribosomes, but can be converted by removal of the linker into a protein
 CC having alpha and beta fragments and being capable of inactivating
 CC eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein
 CC synthesis. They possess a highly specific N-glycosidase activity which
 CC cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S
 CC RNA. RIPs selectively inhibit cellular proliferation of cells, e.g.
 CC cancer cells and HIV-infected T cells. The inactive proRIP proteins make
 CC it possible to provide protein synthesis inhibitors with uses in
 CC practical and improved ways not before possible. The RIP can be used to
 CC make cytotoxic conjugates. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 267 AA;

Query Match 100.0%; Score 1221; DB 2; Length 267;

Best Local Similarity 100.0%; Pred. No. 1e-110; Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSGYGFISNLKRALPNERKLYDIPILRSSLPGSQRYALHILTNVADDT 60
 DB 2 DVSFRLSGATSSGYGFISNLKRALPNERKLYDIPILRSSLPGSQRYALHILTNVADDT 61

QY 61 SVADVTNYIMGYRAGDTSYFFNEASATEAKYVFDARKKTYLPYSGYERLQTPAGK 120
 DB 62 SVADVTNYIMGYRAGDTSYFFNEASATEAKYVFDARKKTYLPYSGYERLQTPAGK 121

QY 121 IRENIPILGLPALDSATTTLPYNNANSASALMWLIQSTSEARARYKFTIEQIGKRVKTF 180
 DB 122 IRENIPILGLPALDSATTTLPYNNANSASALMWLIQSTSEARARYKFTIEQIGKRVKTF 181

QY 181 PSIAITISLENSWSALSKQIQIASTNNQGFESPVLINAQNRVTITNVDAVVTSNIAL 240
 DB 182 PSIAITISLENSWSALSKQIQIASTNNQGFESPVLINAQNRVTITNVDAVVTSNIAL 241

QY 241 LNRRNMA 247
 DB 242 LNRRNMA 248

RESULT 5
 AAW25140
 ID AAW25140 standard; protein; 267 AA.

XX AAW25140;

DT 25-MAR-2003 (revised)
 DT 02-DEC-1997 (first entry)

XX Trichosanthin (a ribosome inhibitory protein) inactive precursor.

XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; barley translation inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A-chain; Saporin; SLT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome.

XX Synthetic.

XX US5646026-A.

XX 08-JUL-1997.

PF 07-JUN-1995; 95US-00485286.
 XX 11-JUN-1990; 90US-00535636.
 PR 09-DEC-1992; 92US-00987927.
 PR 26-JAN-1995; 95US-00378761.
 XX
 PA (DOMC) DOWELANCO.
 XX
 XX Hey TD, Morgan AER, Walsh TA;
 XX
 DR WPI; 1997-362934/33.
 XX
 PT DNA encoding pro-ribosome inactivating proteins - inactive precursors of
 PT ribosome inactivating proteins; can be expressed in eukaryotic cells
 PT without causing cell death.
 XX
 PS Claim 4; Col 115-118; 186pp; English.

CC AAW25140 shows a Trichosanthin (ribosome inhibitory protein, RIP) protein
 CC which was engineered to contain a selectively removable internal peptide
 CC linker sequence separating the alpha and beta units of the RIP. When
 CC separated the two units regain activity and are capable of inactivating
 CC eukaryotic ribosomes and hence preventing protein production. Many
 CC different RIPs may be produced with an internal linker including maize
 CC RIP, Trichosanthin, Ricin A-chain, Abrin-A-chain and Saprotoxin. The Ribs
 CC can be used in the construction of therapeutic toxins targeted to
 CC specific cells such as tumour cells via the attachment of a targeting
 CC polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy
 CC (see USA869903). There is interest in expressing RIP recombinantly in
 CC host eukaryotic cells, because of the capacity to provide correct post-
 CC translational processing. However, RIPs effectively inhibit protein
 CC synthesis in eukaryotic cells resulting in cell death. Since the inactive
 CC RIP proteins are not cytotoxic to eukaryotic cells, they can be
 CC recombinantly expressed in such cells and then converted to active RIP
 CC proteins. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 267 AA;

Query Match 100.0%; Score 1221; DB 2; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1e-110;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPQSGRYALIHLTNYADFTI 60
 DB 2 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPQSGRYALIHLTNYADFTI 61
 QY 61 SVAIDVTNVIYMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120
 DB 62 SVAIDVTNVIYMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 121
 QY 121 IRENIPGLPALDSAITTLFFYNNANSAASALMWLIQSTSEARXYFIEQOIGKRVDTKL 180
 DB 122 IRENIPGLPALDSAITTLFFYNNANSAASALMWLIQSTSEARXYFIEQOIGKRVDTKL 181
 QY 181 PSLAIISLENSWSALSQIOIASTNNGQFESPVLINQONRVTTINVDAGVTSNIALL 240
 DB 182 PSLAIISLENSWSALSQIOIASTNNGQFESPVLINQONRVTTINVDAGVTSNIALL 241
 QY 241 LNRNNMA 247
 DB 242 LNRNNMA 248

RESULT 6

AAB99329 standard; protein; 289 AA.

XX AAB99329;

DT 23-AUG-2001 (first entry)

XX Trichosanthes kirilowii trichosanthin (TCS) protein sequence.

KW Trichosanthes kirilowii; trichosanthin; TCS; mutagenesis; mutation; MTCS;
 KW mutant of trichosanthin; Mongolian snake-gourd; bioactivity; selectivity;
 KW cancer; virus; HIV; metaphase induced labour.
 XX
 OS Trichosanthes kirilowii.

XX Key Location/Qualifiers
 FH Misc-difference 230
 FT /note= "encoded by GCA"

XX CN1283630-A.

XX 14-FEB-2001.

XX 02-AUG-2000; 2000CN-00119553.

XX 02-AUG-2000; 2000CN-00119553.

XX (SHAN-) SHANGHAI INST CYTOBIOLOGY CHINESE ACAD.

XX Ke Y, Nie H;

XX WPI; 2001-291745/31.

XX N-PSDB; AAH41473.

XX Trichosanthin mutant and its preparing process.

XX Disclosure; Page 2 (disclosure); 15pp; Chinese.

CC The present invention describes a trichosanthin mutant which is prepared
 CC through the mutational deformation of the trichosanthin gene and using an
 CC expression system. The trichosanthin gene is isolated from Trichosanthes
 CC kirilowii (Mongolian snake-gourd). The trichosanthin mutant has several
 CC advantages including high bioactivity, high selectivity to target, and
 CC strong kill action to cancer cells, virus and HIV. It can also be used
 CC for metaphase induced labour. The present sequence represents the protein
 CC sequence of wild type trichosanthin which is given in the exemplification
 CC of the present invention

XX Sequence 289 AA;

Query Match 100.0%; Score 1221; DB 4; Length 289;
 Best Local Similarity 100.0%; Pred. No. 1.e-110;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPQSGRYALIHLTNYADFTI 60
 DB 24 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPQSGRYALIHLTNYADFTI 83
 QY 61 SVAIDVTNVIYMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120
 DB 64 SVAIDVTNVIYMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 143
 QY 121 IRENIPGLPALDSAITTLFFYNNANSAASALMWLIQSTSEARXYFIEQOIGKRVDTKL 180
 DB 122 IRENIPGLPALDSAITTLFFYNNANSAASALMWLIQSTSEARXYFIEQOIGKRVDTKL 203
 QY 144 IRENIPGLPALDSAITTLFFYNNANSAASALMWLIQSTSEARXYFIEQOIGKRVDTKL 203
 DB 181 PSLAIISLENSWSALSQIOIASTNNGQFESPVLINQONRVTTINVDAGVTSNIALL 240
 QY 204 PSLAIISLENSWSALSQIOIASTNNGQFESPVLINQONRVTTINVDAGVTSNIALL 263
 QY 241 LNRNNMA 247
 DB 264 LNRNNMA 270

RESULT 7

ABB07660 standard; protein; 289 AA.

XX ABB07660;

DT 20-MAY-2002 (first entry)

[illegible]

```

QY 121 IRENIPGLG.PALDSAITTLFFYNANSASALMWLIQSTSEAAKYFEIQOIGKRVDTFL 180
DB 121 IRENIPGLG.PALDSAITTLFFYNANSASALMWLIQSTSEAAKYFEIQOIGKRVDTFL 180
QY 181 PSLAIIISLNSWSALSQIQIASTNNGQFESPVLINQONRVITITNDAGVTSNIALL 240
DB 181 PSLAIIISLNSWSALSQIQIASTNNGQFETPVVLINQONRVITITNDAGVTSNIALL 240
QY 241 LNRNNMA 247
DB 241 LNRNNMA 247

```

RESULT 9

```

AAR07514
ID AAR07514 standard; protein; 289 AA.

```

```

AC AAR07514;
DT 06-FEB-1991 (first entry)
DE Trichosanthin from Trichosanthus kirilowii.
KM Trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.
XX Trichosanthus kirilowii.
OS Trichosanthus kirilowii.
FH Key Location/Qualifiers
FT Region 1..21
FT /label= "signal peptide"
FT /note= "hydrophobic"

```

```

PN WO9012097-A.
XX

```

```

PD 18-OCT-1990.
XX

```

```

PF 04-APR-1989; 89US-0033184.
XX

```

```

PR 04-APR-1989; 89US-0033184.
XX

```

```

PA (GENE-) GENELABS INC.
XX

```

```

PI Platek M, Chow T, Fry K;
XX

```

```

DR WPI; 1990-334847/44.
XX

```

```

DR N-PSDB; AAQ06343.
XX

```

```

PT Recombinant tri:chosanthin protein - with selective inhibitory effect on
XX viral expression in HIV infected T-cells or monocyte-macrophase.

```

```

PS Example; Fig 4; 102pp; English.
XX

```

```

CC Genomic DNA was isolated from T.kirilowii leaves from Korea and a library
CC was constructed. Clone PD21D was identified as likely to contain a TCS-
CC encoding sequence in its 4kb insert. The deduced amino acid sequence is
CC identical to that of TCS purified from Cantonese T.kirilowii roots,
CC except for 2 conservative substitu-tions, i.e. Thr for Ser at position
CC 211 and Met for Thr at position 224. The Canton protein lacks the last 19
CC C-terminal amino acid residues. See also AAQ06344-006351
XX

```

```

SQ Sequence 289 AA;

```

```

Query Match 99.3%; Score 1212; DB 2; Length 289;

```

```

Best Local Similarity 99.2%; Pred. No. 8.5e-110;
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORVALIHLTNVADETI 60
DB 24 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORVALIHLTNVADETI 83
QY 61 SVADIVTNVYIMGYRAGDTSYFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTPAAG 120
DB 61 SVADIVTNVYIMGYRAGDTSYFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTPAAG 120

```

```

DB 84 SVADIVTNVYIMGYRAGDTSYFNEASATEAKYVFKDAMRKVTLPYSGNYERLQTPAAG 143
QY 121 IRENIPGLG.PALDSAITTLFFYNANSASALMWLIQSTSEAAKYFEIQOIGKRVDTFL 180
DB 144 IRENIPGLG.PALDSAITTLFFYNANSASALMWLIQSTSEAAKYFEIQOIGKRVDTFL 203
QY 181 PSLAIIISLNSWSALSQIQIASTNNGQFESPVLINQONRVITITNDAGVTSNIALL 240
DB 204 PSLAIIISLNSWSALSQIQIASTNNGQFETPVVLINQONRVITITNDAGVTSNIALL 263
QY 241 LNRNNMA 247
DB 241 LNRNNMA 247

```

RESULT 10

```

AAR25572
ID AAR25572 standard; protein; 289 AA.

```

```

AC AAR25572;
XX

```

```

DT 25-MAR-2003 (revised)
XX

```

```

DT 13-JAN-1993 (first entry)
XX

```

```

DE Trichosanthin from Trichosanthus kirilowii.
XX

```

```

KM TCS; alpha-trichosanthin; Radix trichosanthin; abortifacient;
XX ribosome inactivating protein; RIP; HIV-infected human T cells;
XX human immunodeficiency virus.

```

```

KW Trichosanthus kirilowii.
XX

```

```

OS Trichosanthus kirilowii.
XX

```

```

FH Key Location/Qualifiers
XX

```

```

FT Misc-difference 57
FT /note= "Leu in previously published sequence"

```

```

FT Misc-difference 60
FT /note= "Ile in previously published sequence"

```

```

FT Misc-difference 72
FT /note= "Ile in previously published sequence"

```

```

FT Misc-difference 82..84
FT /note= "region not present in previously published
sequence"

```

```

FT Misc-difference 92..93
FT /note= "previously published sequence contained a 10
amino acid insert (DAGLPRNAVTL) between Val and Tyr"

```

```

FT Misc-difference 143
FT /note= "Gly in previously published sequence"

```

```

FT Misc-difference 144
FT /note= "Leu in previously published sequence"

```

```

FT Misc-difference 196
FT /note= "Ser in previously published sequence"

```

```

FT Misc-difference 214..215
FT /note= "previously published sequence contained a Leu
inserted between Ser and Trp"

```

```

FT Misc-difference 216
FT /note= "Leu in previously published sequence"

```

```

FT Misc-difference 231
FT /note= "Thr in previously published sequence"

```

```

FT Misc-difference 234
FT /note= "Ser in directly sequenced TCS"

```

```

FT Misc-difference 246..266
FT /note= "21 amino acids not present in previously
published sequence"

```

```

FT Misc-difference 247
FT /note= "Thr in directly sequenced TCS"

```

```

FT US5128460-A.
XX

```

```

PD 07-JUL-1992.
XX

```

```

XX 04-APR-1990; 90US-00504775.
XX

```

```

PF 04-APR-1990; 89US-0033184.
XX

```

```

PR 04-APR-1989;

```

PR 07-SEP-1989; 89US-00404326.
 XX (GENE-) GENELABS INC.
 XX
 XX
 PI Platak M, Chow TP, Fry K;
 XX
 DR WPI; 1992-249485/30.
 XX N-PSDB; AAQ26499.
 PT
 PT Nucleic acid encoding trichosanthin protein - which can be used to
 PT inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV
 PT expression.

Claim 1; Fig 4; 53pp; English.

XX Trichosanthin protein was isolated from T.kirlowii root tuber and
 CC sequenced. The amino acid sequence was used to design sets of degenerate
 CC primers (see AAQ26506-8) for PCR amplification of the TCS coding
 CC sequence. The amplified product was used as a probe to isolate TCS coding
 CC sequence from T.kirlowii genomic libraries. One clone (pQ21D) contained
 CC a 4kb insert. The amino acid sequence deduced from the pQ21D insert
 CC differed from the purified TCS sequence by conservative substitutions at
 CC two positions (see Features Table). The differences are postulated to
 CC indicate minor variations between strains; the purified TCS was obtained
 CC from the Canton region of China and the genomic DNA was obtained from
 CC T.kirlowii leaves from Korea. The amino acid sequence was also found to
 CC differ substantially from the previously published TCS sequence (Acta
 CC Chemica Sinica, 43:1943, 1984 and Pure and Appl. Chem., 58(5):789, 1986).
 CC The differences are shown in the Features Table. The present sequence
 CC agrees closely with X-ray diffraction data on crystallized TCS. The 21-
 CC amino acid insert also provides greater sequence homology with a number
 CC of RIPS such as ricin A chain and abrin A chain than the previously
 CC published sequence. (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 289 AA;

XX Query Match 99.3%; Score 1212; DB 2; Length 289;

XX Best Local Similarity 99.2%; Pred. No. 8.5e-110; Mismatches 1; Indels 0; Gaps 0;

XX Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSPLPSGORYALHLTNVADETI 60
 XX
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSPLPSGORYALHLTNVADETI 83
 XX
 QY 61 SVAIDVTNVIYIMGRAGDTSYFFNEASATEAAKYVFKDMARKVTLPYSGYERLQTPAAGK 120
 XX
 DB 84 SVAIDVTNVIYIMGRAGDTSYFFNEASATEAAKYVFKDMARKVTLPYSGYERLQTPAAGK 143
 XX
 QY 121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFIHQIGKRVDTFL 180
 XX
 DB 144 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFIHQIGKRVDTFL 203
 XX
 QY 181 PSIAITISLNSWSALSKQIQIASTNNGQFESPVLINAONORVTTINVDAGVTSNIAL 240
 XX
 DB 204 PSIAITISLNSWSALSKQIQIASTNNGQFETPVLLINAONORVTTINVDAGVTSNIAL 263
 XX
 QY 241 LNRNNMA 247
 XX
 DB 264 LNRNNMA 270
 XX

XX RESULT 11

XX ID AAR29272 standard; protein; 289 AA.

XX AC AAR29272;

XX DT 25-MAR-2003 (revised)

XX DT 16-APR-1993 (first entry)

XX DE Trichosanthin protein (encoded by pQ21D).

KM TCS; alpha-trichosanthin; Radix-trichosanthin; primer; inhibition;
 KM viral expression; HIV; T-cell; macrophage.
 XX
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 XX Peptide 1..23
 FT /label= sig peptide
 FT /note= "putative N-terminal extension of the mature TCS"

FT Protein 24..270
 FT /label= mat_protein

FT Misc-difference 234
 FT /note= "plant-derived TCS has Ser at this position"

FT Misc-difference 247
 FT /note= "plant-derived TCS has Thr at this position"

FT Protein 270..289
 FT /note= "putative C-terminal extension of the mature TCS"

PN US5166056-A.

PN 24-NOV-1992.

PD 24-NOV-1992.

PF 09-DEC-1991; 91US-00804293.

XX 04-APR-1989; 89US-00331184.

PR 07-SEP-1989; 89US-00404326.

XX (GENE-) GENELABS INC.

XX Platak M, Chow TP;

XX WPI; 1992-414954/50.

XX Recombinant Trichosanthin protein prodn. in E. coli - for use in the

XX selective inhibition of viral expression in HIV infected cells.

XX Disclosure; Fig 4; 37pp; English.

XX The sequence is identical to that of plant-derived TCS except for two
 CC conservative changes: a Thr for a Ser substitution at position 21 and a
 CC Met for a Thr substitution at position 224. TCS is likely produced as a
 CC secreted protein that undergoes post-translational processing at both the
 CC amino and carboxy ends. The TCS coding sequence was amplified using the
 CC primers of AAQ31828-30. The amplified prod. has the sequence of AAQ31827,
 CC which was used as a probe. One isolate, pQ21D, comprises the sequence of
 CC AAQ31826. The recombinant TCS sequence may be used in the recombinant
 CC prodn. of TCS. TCS can be used for the selective inhibition of viral
 CC expression in HIV-infected human T-cells or macrophages. (Updated on 25-
 CC MAR-2003 to correct PF field.)

XX Sequence 289 AA;

XX Query Match 99.3%; Score 1212; DB 2; Length 289;

XX Best Local Similarity 99.2%; Pred. No. 8.5e-110; Mismatches 1; Indels 0; Gaps 0;

XX Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSPLPSGORYALHLTNVADETI 60
 XX
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSPLPSGORYALHLTNVADETI 83
 XX
 QY 61 SVAIDVTNVIYIMGRAGDTSYFFNEASATEAAKYVFKDMARKVTLPYSGYERLQTPAAGK 120
 XX
 DB 84 SVAIDVTNVIYIMGRAGDTSYFFNEASATEAAKYVFKDMARKVTLPYSGYERLQTPAAGK 143
 XX
 QY 121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFIHQIGKRVDTFL 180
 XX
 DB 144 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKFIHQIGKRVDTFL 203
 XX
 QY 181 PSIAITISLNSWSALSKQIQIASTNNGQFESPVLINAONORVTTINVDAGVTSNIAL 240
 XX
 DB 204 PSIAITISLNSWSALSKQIQIASTNNGQFETPVLLINAONORVTTINVDAGVTSNIAL 263
 XX
 QY 241 LNRNNMA 247
 XX

Db 264 INRNMA 270

RESULT 12

AAR32986
ID AAR32986 standard; protein; 289 AA.

XX AAR32986;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 17-JUN-1993 (first entry)

DE Encodes chinese cucumber alpha-tricosanthin.
XX
XX Recombinant products; commercial production; fermentation; biosynthesis;
KW natural products; recombinant proteins; product expression;
KW protein expression; expressed proteins.

OS Cucurbitaceae.

XX MO3033161-A1.

XX 18-FEB-1993.

PF 31-JUL-1992; 92WC-US006359.

XX 01-AUG-1991; 91US-00739143.

XX (DONS/) DONSON J.

PA (DAMS/) DAWSON W O.

PA (GRAN/) GRANTHAM G L.

PA (TURP/) TURPEN T H.

PA (GARG/) GARGER S J.

PA (GRIL/) GRILLE L K.

XX Donson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM,

PI Garger SJ, Grille LK,

XX WPI, 1993-076518/09.

DR N-PSDB; AAQ37679.

XX Recombinant plant viral nucleic acids - used to express a prod., e.g.

PT antibody or IL-1 in a plant.

XX Example 4; Page 96; 30pp; English.

XX This sequence represents chinese cucumber alpha-tricosanthin. The coding

CC sequence is inserted into a recombinant plant viral nucleic acid which is

CC then used to express a recombinant product (in this case alpha-

CC tricosanthin) in a plant. The plant viral sequence may be from tobacco

CC mosaic, cucumber green mottle, cowpea mosaic, brome mosaic, broad bean

CC mottle, rice necrosis, geminiviruses, tomato golden mosaic, Cassava

CC latent and maize streak viruses. (Updated on 25-MAR-2003 to correct PN

CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-

XX 2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

SQ Sequence 289 AA;

Query Match 99.3%; Score 1212; DB 2; Length 289;

Best Local Similarity 99.2%; Pred. No. 8.5e-110;

Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRUGATSSSYGVFINLRKALPNERKLYDIPILRSSLPSSQRYALIHILTNVADETI 60

DB 24 DVSFRUGATSSSYGVFINLRKALPNERKLYDIPILRSSLPSSQRYALIHILTNVADETI 83

QY 61 SVADIVTNYINGYRAGDTSYFNEASATEAAKYVKDMARKTLLPYSGNYEHLQTAAGK 120

DB 84 SVADIVTNYINGYRAGDTSYFNEASATEAAKYVKDMARKTLLPYSGNYEHLQTAAGK 143

QY 121 IRENIPLGLPALSATITLTFYNNANSASALMWLIQSTSEARXYKFEQIGKRVDTFL 180

DB 144 IRENIPLGLPALSATITLTFYNNANSASALMWLIQSTSEARXYKFEQIGKRVDTFL 203

QY 181 PSLATISLENSWSALSKOIQIASTNNQGFESRPVYLINONQRYVTNNVADGVTSNIAL 240

DB 204 PSLATISLENSWSALSKOIQIASTNNQGFETPVVLINONQRYVTNNVADGVTSNIAL 263

QY 241 INRNMA 247

DB 264 INRNMA 270

RESULT 13

AAR55129
ID AAR55129 standard; protein; 289 AA.

XX AAR55129;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 11-JAN-1995 (first entry)

DE Alpha-trichosanthin coding.

XX Virus; recombinant; plant virus; alpha trichosanthin; phenotype;

KW alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus;

KW rice necrosis virus tobamovirus; gene expression; chinese cucumber.

XX Trichosanthin kilowil.

XX US5316931-A.

XX 31-MAY-1994.

PF 31-JUL-1992; 92US-00923692.

XX 26-FEB-1988; 88US-00160766.

PR 26-FEB-1988; 88US-00160771.

PR 15-JUL-1988; 88US-00219279.

PR 17-FEB-1988; 88US-00310881.

PR 05-MAY-1989; 89US-00347637.

PR 08-JUN-1989; 89US-00363138.

PR 22-OCT-1990; 90US-00600244.

PR 16-JAN-1991; 91US-00641617.

PR 26-JUL-1991; 91US-00737889.

PR 01-AUG-1991; 91US-00739143.

XX (BIOS-) BIOSOURCE GENETICS CORP.

XX Garger SJ, Turpen AM, Grille LK, Grantman GL, Dawson WO, Donson J;

PI Turpen TH;

XX WPI, 1994-176269/21.

DR N-PSDB; AAQ65573.

XX New recombinant plant viral nucleic acid - capable of systemic infection

PT and stable expression of non-native nucleic acid in plant host.

XX Example 4; Col 47-50; 44pp; English.

XX The alpha-trichosanthin gene may be inserted into a recombinant plant

CC virus which can then be used to infect plants for the production of non-

CC native products (in this case alpha-trichosanthin). Other genes which

CC may be inserted into the virus are those which control a phenotypic

CC trait, such as male sterility, or sequences encoding anti-sense RNA which

CC can be useful to prevent the expression of undesired phenotypic traits.

CC The recombinant virus is derived from a plus sense, single stranded virus

CC selected from tobamovirus, brome mosaic virus, rice necrosis virus or a

CC gemini virus. (Updated on 25-MAR-2003 to correct PF field.) (Updated on

XX 27-AUG-2003 to correct OS field.)

SQ Sequence 289 AA;

Query Match 99.3%; Score 1212; DB 2; Length 289;
 Best Local Similarity 99.2%; Pred. No. 8.5e-110;
 Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSLSPGSOYALHILTNVADETI 60
 DB 24 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSLSPGSOYALHILTNVADETI 83

QY 61 SVADVTNVIYIMGYRAGDTSYFFNEASATEAAKYVKDMARKYTLPSGNYERLQTPACK 120
 DB 84 SVADVTNVIYIMGYRAGDTSYFFNEASATEAAKYVKDMARKYTLPSGNYERLQTPACK 143

QY 121 IRENIPILGIPALDSATITLTFYVYANSAASALMWLIQSTSEAAKYKFEIQOIGKRVDTFL 180
 DB 144 IRENIPILGIPALDSATITLTFYVYANSAASALMWLIQSTSEAAKYKFEIQOIGKRVDTFL 203

QY 181 PSIAITISLNSWSALSQKQIQAISTNNGQFESPVVLINAQNRVTITNVDAVVTSNIAL 240
 DB 204 PSIAITISLNSWSALSQKQIQAISTNNGQFETPVVLINAQNRVTITNVDAVVTSNIAL 263

QY 241 LNRNNMA 247
 DB 264 LNRNNMA 270

RESULT 14
 AAM10468
 ID AAM10468 standard; protein; 289 AA.
 AC AAM10468;
 XX
 XX 17-OCT-2003 (revised)
 DT 26-APR-1997 (first entry)
 XX
 DE Chinese cucumber alpha-trichosanthin.
 XX
 KM Recombinant viral nucleic acid; RNA virus; vector; tobacco mosaic virus;
 KM TMV; Chinese cucumber; alpha-trichosanthin;
 KM ribosome inactivating protein; antiviral; virucide; transgenic plant.
 XX
 OS Trichosanthes kirilowii; Maximowicz.
 XX
 XX MO9640867-A1.
 PN 19-DEC-1996.
 PD
 XX
 PF 06-JUN-1996; 96MO-US009299.
 PR 07-JUN-1995; 95US-00483502.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Donson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM;
 PI Garger SJ, Grill LK;
 XX
 DR WPI; 1997-065181/06.
 DR N-PSDB; AAT47094.
 XX
 PT Recombinant viral nucleic acid producing, e.g. male sterility in plants -
 PT comprises nucleic acid whose transcription is controlled by another
 PT sequence.
 PT
 XX
 XX Example 4; Page 124-125; 149pp; English.
 XX
 CC Chinese cucumber alpha-trichosanthin (AAM10468) is a ribosome
 CC inactivating protein of potential use in the treatment of HIV infection.
 CC Expression vector pBCG152 was constructed in which the alpha-
 CC trichosanthin coding sequence (see also AAT47094) was placed under
 CC control of the promoter of the tobacco mosaic virus-U1 coat protein gene,
 CC which had been deleted. The viral nucleic acid was capable of self-
 CC replication, encapsidation and systemic spread in infected Nicotiana
 CC benthamiana plants, and directed the high-level expression of

CC biologically active alpha-trichosanthin in plant tissues. (Updated on 17-
 CC OCT-2003 to standardise OS field)
 CC
 SQ Sequence 289 AA;

Query Match 99.3%; Score 1212; DB 2; Length 289;
 Best Local Similarity 99.2%; Pred. No. 8.5e-110;
 Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSLSPGSOYALHILTNVADETI 60
 DB 24 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSLSPGSOYALHILTNVADETI 83

QY 61 SVADVTNVIYIMGYRAGDTSYFFNEASATEAAKYVKDMARKYTLPSGNYERLQTPACK 120
 DB 84 SVADVTNVIYIMGYRAGDTSYFFNEASATEAAKYVKDMARKYTLPSGNYERLQTPACK 143

QY 121 IRENIPILGIPALDSATITLTFYVYANSAASALMWLIQSTSEAAKYKFEIQOIGKRVDTFL 180
 DB 144 IRENIPILGIPALDSATITLTFYVYANSAASALMWLIQSTSEAAKYKFEIQOIGKRVDTFL 203

QY 181 PSIAITISLNSWSALSQKQIQAISTNNGQFESPVVLINAQNRVTITNVDAVVTSNIAL 240
 DB 204 PSIAITISLNSWSALSQKQIQAISTNNGQFETPVVLINAQNRVTITNVDAVVTSNIAL 263

QY 241 LNRNNMA 247
 DB 264 LNRNNMA 270

RESULT 15
 AAM11870
 ID AAM11870 standard; protein; 289 AA.
 AC AAM11870;
 XX
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-APR-1997 (first entry)
 XX
 DE Chinese cucumber alpha-trichosanthin.
 XX
 KM Recombinant virus; alpha-haemoglobin; human; chinese cucumber;
 KM alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin;
 KM subgenomic promoter; coat protein.
 XX
 OS Cucumis sp.
 XX
 PN US5589367-A.
 PD 31-DEC-1996.
 XX
 PF 19-JAN-1994; 94US-00184237.
 PR 26-FEB-1988; 88US-00160766.
 PR 26-FEB-1988; 88US-00160771.
 PR 15-JUL-1988; 88US-00219279.
 PR 17-FEB-1989; 89US-00310881.
 PR 05-MAY-1989; 89US-00347637.
 PR 08-JUN-1989; 89US-00363138.
 PR 22-OCT-1990; 90US-00600244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.
 PR 31-JUL-1992; 92US-00923692.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Garger SJ, Turpen AM, Grill LK, Grantham GL, Donson J, Dawson WO;
 PI Turpen TH;
 XX
 DR WPI; 1997-076845/07.
 DR N-PSDB; AAT61376.

XX Recombinant viral DNA for altering plant phenotype or protein prodn -
PT contains non-native sub-genomic promoter for expression of heterologous
PT protein and native promoter for expression of coat protein.
XX

PS Example 4; Col 45-46; 42pp; English.

CC The sequences given in AM11868-71 represent proteins which were produced
CC by the recombinant viruses of the invention. The viruses are recombinant
CC plant viruses which comprise a native plant virus subgenomic promoter, at
CC least one non-native plant virus subgenomic promoter, and a sequence
CC encoding a plant virus coat protein. These heterologous sequences are
CC preferably under the control of the native promoter sequence. By using a
CC plant virus existing cells can be altered with a new coding sequences
CC without involving germ cell. The recombinant viruses are stable and can
CC cause systemic infection, with stable expression/transcription in plants
CC that are hosts for the non-native part of the vector. The nucleotide
CC sequences encoding these protein preferably integrated in plant viruses
CC having either the O-coat protein or the UI-coat protein gene. (Updated on
CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC field.) (Updated on 27-AUG-2003 to correct OS field.)
XX

SQ Sequence 289 AA;

Query Match 99.3%; Score 1212; DB 2; Length 289;

Best Local Similarity 99.2%; Pred. No. 8.5e-110; Indels 0; Gaps 0;

Matches 245; Conservative 1; Mismatches 1;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPILRSSLPQSQRYALIHLTNYADETI 60
DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPILRSSLPQSQRYALIHLTNYADETI 83
QY 61 SVAIDVTNYINGYRAGDTSYFENEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120
DB 84 SVAIDVTNYINGYRAGDTSYFENEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGK 143
QY 121 IRENIPLGIPALDSAITTLFYYNANSASALMWLIQSTSEAAKYKPIEQQIGKRVDTFL 180
DB 144 IRENIPLGIPALDSAITTLFYYNANSASALMWLIQSTSEAAKYKPIEQQIGKRVDTFL 203
QY 181 PSLAIIISLENSWSALSQIQIASTNNGQESPVLINAONORTITNVDAGVTSNIALL 240
DB 204 PSLAIIISLENSWSALSQIQIASTNNGQETPVVLIINAONORTITNVDAGVTSNIALL 263
QY 241 LNRNNMA 247
DB 264 LNRNNMA 270

Search completed: April 12, 2005, 15:10:00
Job time : 112.519 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2005, 14:57:02 ; Search time 25.3451 Seconds

(without alignment) 937.676 Million cell updates/sec

Title: US-09-905-247A-8

Perfect score: 1221

Sequence: 1 DVSPRLSGATSSSYGVFIN.....VDAGVTSNALLLNRMNA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pirl:*

2: pirl:*

3: pirl:*

4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1221	100.0	289	1	RLTUT	rRNA N-glycosidase
2	1194	97.8	247	2	JU0393	karsaurin - Mongol
3	1194	97.8	289	2	JU0506	karsaurin C - Tric
4	1189	97.4	247	2	JU0503	karsaurin-B - Tric
5	802	65.7	286	1	RLPUGG	rRNA N-glycosidase
6	754	61.8	277	2	S22494	beta-luffin - smoo
7	728.5	59.7	278	2	S23519	rRNA N-glycosidase
8	709	58.1	286	2	S25560	rRNA N-glycosidase
9	706	57.8	286	2	JU0435	luffin-B - smooth
10	680	55.7	250	2	JU0108	rRNA N-glycosidase
11	665.5	54.6	245	2	JU0480	ricin D precursor
12	421	34.5	576	1	RLCSAG	agglutinin precurs
13	396.5	32.5	564	1	RLCSAG	abrin (clone 7.2)
14	352	28.1	528	2	S32431	abrin-d precursor
15	343	28.1	562	2	S16022	abrin-c precursor
16	343	28.1	562	2	S32430	abrin-b precursor
17	340.5	27.9	527	2	S32430	abrin-a precursor
18	336	27.5	528	1	TZLSA	agglutinin I precu
19	335.5	27.5	570	2	S62627	mistletoe lectin I
20	325	26.6	254	2	PD0018	rRNA N-glycosidase
21	321	26.3	316	2	JU0753	betanulin - beet
22	266.5	21.8	272	2	JU0481	rRNA N-glycosidase
23	261	21.4	313	2	S17757	rRNA N-glycosidase
24	258.5	19.7	261	2	S28421	antiviral protein
25	240.5	15.6	310	2	S46239	ribosome-inactivat
26	190.5	15.3	289	2	A39817	rRNA N-glycosidase
27	187	13.9	289	2	T12573	rRNA N-glycosidase
28	169.5	13.8	45	2	A39598	TAP-29 anti-HIV pr

30	163.5	13.4	253	2	S28542	rRNA N-glycosidase
31	163.5	13.4	253	2	A58923	rRNA N-glycosidase
32	162.5	13.3	253	2	S28539	rRNA N-glycosidase
33	159.5	13.1	253	2	S28541	rRNA N-glycosidase
34	158.5	13.0	283	2	S05205	rRNA N-glycosidase
35	157.5	12.9	292	1	RLQHG2	rRNA N-glycosidase
36	156.5	12.8	253	2	S29931	rRNA N-glycosidase
37	155	12.7	293	2	S17519	rRNA N-glycosidase
38	153	12.5	43	2	S16491	rRNA N-glycosidase
39	142.5	11.7	236	2	S17932	rRNA N-glycosidase
40	140.5	11.5	106	2	B39761	abrin (clone 3.7)
41	122	10.0	280	1	RLBH	rRNA N-glycosidase
42	119	9.7	280	2	JU0548	protein synthesis
43	118	9.7	281	2	B38664	30k ribosome inact
44	111.5	9.1	319	2	I76713	variant shiga-like
45	111.5	9.1	319	2	S58343	Shiga-like toxin I

ALIGNMENTS

RESULT 1

RLTUT
rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian
N/Alternate names: alpha-TCS; type I ribosome-inactivating protein
C/Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C/Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text change 09-Jul-2004
C/Accession: JU0566; A36274; JU093; A36274; JU0003
R/Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.
Gene 97, 267-272, 1991
A/Title: Cloning of trichosanthin cDNA and its expression in *Escherichia coli*.
A/Reference number: JU0566; PMID:91153657; PMID:1899291
A/Accession: JU0566
A/Molecule type: mRNA
A/Residues: 1-289 <SHA>
A/Cross-references: UNIPROT:P09989; GB:M34858; NID:G170536; PIDN:AAA4207.1; PID:G170537
A/Experimental source: tuber
R/Chow, T.P.; Feldman, R.A.; Lovett, M.; Platak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A/Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rhl
A/Reference number: A36274; PMID:90256790; PMID:2341400
A/Accession: A36274
A/Molecule type: DNA
A/Residues: 1-233, 'T', 235-246, 'W', 248-289 <CHD>
A/Cross-references: GB:J05434; NID:G170534; PIDN:AAA34206.1; PID:G170535
R/Cheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
Acta Genet. Sin. 21, 42-51, 1994
A/Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A/Reference number: JU0093; PMID:94271613; PMID:8003348
A/Accession: JU0093
A/Molecule type: DNA
A/Residues: 1-77, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>
R/Cross-references: GB:S70176; NID:G547148; PIDN:AAA31048.1; PID:G547149
J. Biol. Chem. 265, 8665-8669, 1990
U. Collins, E.J.; Roberts, J.D.; Lopresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwar
A/Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abri
A/Reference number: A36273; PMID:90256789; PMID:2341399
A/Accession: A36273
A/Molecule type: protein
A/Residues: 24-270 <COL>
R/Huang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Y.
Pure Appl. Chem. 58, 789-798, 1996
A/Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
A/Reference number: JU0003
A/Accession: JU0003
A/Molecule type: protein
A/Residues: 24-56, 'L', 58-59, 'I', 61-71, 'I', 73-81, 85-86, 'L', 88-92, 'DAGLPKNAV', 93-142, 'GI'
R/Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A/Reference number: A67091; PDB:IMR1
A/Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-
R/Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.

submitted to the Brookhaven Protein Data Bank, July 1994
 A:Reference number: A67092; PDB:IMRK
 A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24
 R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
 submitted to the Brookhaven Protein Data Bank, December 1994
 A:Reference number: A66711; PDB:ITCS
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
 R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
 Nat. Struct. Biol. 1, 695-700, 1994
 A:Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
 A:Reference number: A56822; PMID:95560714; PMID:7534073
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms
 A:Comment: Alpha-trichosanthin has been used to induce abortions.
 A:Genetics:
 A:Gene: tcs
 A:Function:
 A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA then
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 C:Keywords: abortifacient; glycosidase; hydrolase; root; toxin
 F:1-23/Domain: signal sequence #status predicted <Sig>
 F:24-270/Product: trichosanthin alpha #status experimental <Mat>
 F:27-266/Domain: rRNA N-glycosidase homology <RMG>
 F:271-289/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:93,183,186/Active site: Tyr, Glu, Arg #status predicted

Query Match 100.0%; Score 1221; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 3; 7e-95;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPILRSSPGSQRYALIHNTYADETI 60
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPILRSSPGSQRYALIHNTYADETI 83
 QY 61 SVAIDVTNVIYMGYRAGDTSYFFNESAATEAKYFKDAMRKVTLPYSGNVERLQTAAGK 120
 DB 84 SVAIDVTNVIYMGYRAGDTSYFFNESAATEAKYFKDAMRKVTLPYSGNVERLQTAAGK 143
 QY 121 IRENIPGLG.PALDSATITLTFYNNANSASALMWLQSTSEARRYFEIQIGKRVDTKL 180
 DB 144 IRENIPGLG.PALDSATITLTFYNNANSASALMWLQSTSEARRYFEIQIGKRVDTKL 203
 QY 181 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINANORVTTTNVDAGVTSNIALL 240
 DB 204 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINANORVTTTNVDAGVTSNIALL 263
 QY 241 LNRNNMA 247
 DB 264 LNRNNMA 270

RESULT 2
 J00393
 karasurin - Mongolian snake-gourd
 C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: J00393; PS0163
 R:Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.
 Chem. Pharm. Bull. 39, 1244-1249, 1991
 A:Title: The complete amino acid sequence of an abortifacient protein, karasurin.
 A:Reference number: J00393; PMID:92005921; PMID:1914000
 A:Accession: J00393
 A:Molecule type: protein
 A:Residues: 1-247 <TOY>
 A:Cross-references: UNIPROT:P24478
 A:Note: a sequence which lacks Ala-247 is also shown in this publication
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 C:Keywords: abortifacient
 F:4-243/Domain: rRNA N-glycosidase homology <RMG>

Query Match 97.8%; Score 1194; DB 2; Length 247;
 Best Local Similarity 97.6%; Pred. No. 5; 5e-93;
 Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPILRSSPGSQRYALIHNTYADETI 60
 DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPILRSSPGSQRYALIHNTYADETI 60
 QY 61 SVAIDVTNVIYMGYRAGDTSYFFNESAATEAKYFKDAMRKVTLPYSGNVERLQTAAGK 120
 DB 61 SVAIDVTNVIYMGYRAGDTSYFFNESAATEAKYFKDAMRKVTLPYSGNVERLQTAAGK 120
 QY 121 IRENIPGLG.PALDSATITLTFYNNANSASALMWLQSTSEARRYFEIQIGKRVDTKL 180
 DB 121 IRENIPGLG.PALDSATITLTFYNNANSASALMWLQSTSEARRYFEIQIGKRVDTKL 180
 QY 181 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINANORVTTTNVDAGVTSNIALL 240
 DB 181 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINANORVTTTNVDAGVTSNIALL 240
 QY 241 LNRNNMA 247
 DB 241 LNRNNMA 247

RESULT 3
 J05606
 karasurin C - Trichosanthes kirilowii var. japonica
 N:Contains: karasurin A
 C:Species: Trichosanthes kirilowii var. japonica
 C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
 C:Accession: J05606; J05033
 R:Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.
 Biol. Pharm. Bull. 20, 711-713, 1997
 A:Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote
 A:Reference number: J05606; PMID:97356562; PMID:9212998
 A:Accession: J05606
 A:Molecule type: DNA
 A:Residues: 1-289 <MIZ>
 A:Cross-references: UNIPROT:P24478; DDBJ:AB000666; NID:G2329830; PIDN:BAA21786.1; PID:92
 R:Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
 Biol. Pharm. Bull. 19, 1485-1489, 1996
 A:Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
 A:Reference number: J05032; PMID:97108848; PMID:8951169
 A:Accession: J05033
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 22-270 <KON>
 C:Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 F:22-270/Product: karasurin C #status predicted <MAC>
 F:24-270/Product: karasurin A #status predicted <MAA>
 F:27-266/Domain: rRNA N-glycosidase homology <RMG>

Query Match 97.8%; Score 1194; DB 2; Length 289;
 Best Local Similarity 97.6%; Pred. No. 6; 9e-93;
 Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPILRSSPGSQRYALIHNTYADETI 60
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKYDIPILRSSPGSQRYALIHNTYADETI 83
 QY 61 SVAIDVTNVIYMGYRAGDTSYFFNESAATEAKYFKDAMRKVTLPYSGNVERLQTAAGK 120
 DB 84 SVAIDVTNVIYMGYRAGDTSYFFNESAATEAKYFKDAMRKVTLPYSGNVERLQTAAGK 143
 QY 121 IRENIPGLG.PALDSATITLTFYNNANSASALMWLQSTSEARRYFEIQIGKRVDTKL 180
 DB 144 IRENIPGLG.PALDSATITLTFYNNANSASALMWLQSTSEARRYFEIQIGKRVDTKL 203
 QY 181 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINANORVTTTNVDAGVTSNIALL 240
 DB 204 PSLAIIISLNSWSALSKOIQIASTNNGOFESPVLINANORVTTTNVDAGVTSNIALL 263
 QY 241 LNRNNMA 247

Db 264 LNENMMA 270

RESULT 4

UC5032
 karasurin-B - Trichosanthes kirilowii var. japonica
 C/Species: Trichosanthes kirilowii var. japonica
 C/Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
 C/Accession: J05032
 R/Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
 Biol. Pharm. Bull. 19, 1485-1489, 1996
 A/Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
 A/Reference number: J05032; PMID:97108848; PMID:89511169
 A/Accession: J05032
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-247 <MON>
 A/Cross-references: UNIPROT:Q41216; UNIPROT:Q94KE4; UNIPROT:O8LPV7
 C/Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyze
 C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 F/4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match 97.4%; Score 1189; DB 2; Length 247;
 Best Local Similarity 97.2%; Pred. No. 1.5e-92;
 Matches 240; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSGYGFISMLRKALPNERKLYDIPILRSGLPGSQRYALHLNVADETI 60
 |||||
 Db 1 DVSFRLSGATSSGYGFISMLRKALPNERKLYDIPILRSGLPGSQRYALHLNVADETI 60
 QY 61 SVADVTNYYIMGYRADGTSYFPNEASATEAAKYVFDAMRKYTLPPSGYERLQTAAGK 120
 |||||
 Db 61 SVADVTNYYIMGYRADGTSYFPNEASATEAAKYVFDAMRKYTLPPSGYERLQTAAGK 120
 QY 121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSAARAKYFIEQIIGKRVDTFL 180
 |||||
 Db 121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSAARAKYFIEQIIGKRVDTFL 180
 QY 121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSAARAKYFIEQIIGKRVDTFL 180
 |||||
 Db 121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSAARAKYFIEQIIGKRVDTFL 180
 QY 181 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAOQRVTITNVDAVGTSTNIAL 240
 |||||
 Db 181 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAOQRVTITNVDAVGTSTNIAL 240
 QY 241 LNENMMA 247
 |||||
 Db 241 LNENMMA 247

RESULT 5

RLPUG
 rRNA N-glycosidase (EC 3.2.2.22) alpha-momorcharin precursor [validated] - balsam pear
 N/Alternate names: agglutinin; momordin-A; ribosome-inactivating protein momorcharin alif
 C/Species: Momordica charantia (balsam pear, bitter melon)
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C/Accession: S14273; A61318; S16490; J06628; S01670
 R/Ho, W.K.K.; Liu, S.C.; Shaw, P.C.; Yeung, H.W.; Ng, T.B.; Chan, W.Y.
 Biochim. Biophys. Acta 1088, 311-314, 1991
 A/Title: Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating protein.
 A/Reference number: S14273; PMID:91159486; PMID:2001404
 A/Accession: S14273
 A/Molecule type: mRNA
 A/Residues: 1-286 <HOW>
 A/Cross-references: UNIPROT:P16094; EMBL:X57682; NID:G19527; PIDD:CAA40869.1; PIDD:G19528
 R/Li, S.S.L.
 Experientia 36, 524-527, 1980
 A/Title: Purification and partial characterization of two lectins from Momordica charantia
 A/Reference number: A61318; PMID:80201763; PMID:7379938
 A/Accession: A61318
 A/Molecule type: protein
 A/Residues: 24-50 <LUA>
 A/Note: as a lectin shows agglutinating activity for type-O red blood cells
 R/Montecucchi, P.C.; Lazzerini, A.M.; Barbieri, L.; Stipre, F.; Soria, M.; Lappt, D.
 Int. J. Pept. Protein Res. 33, 263-267, 1989
 A/Title: N-terminal sequence of some ribosome-inactivating proteins.

A/Reference number: S16331; PMID:89326691; PMID:2753596

A/Accession: S16490

A/Molecule type: protein

A/Residues: 24-68,'X',70 <MON>

R/Mizumoto, Y.; Funatsu, G.

Biosci. Biotechnol. Biochem. 57, 1141-1144, 1993

A/Title: The complete amino acid sequence of momordin-a, a ribosome-inactivating protei

A/Reference number: J06628; PMID:93372465; PMID:7763984

A/Accession: J06628

A/Molecule type: protein

A/Residues: 24-107,'Q',109-123,125-147,'L',149-154,'I',156-205,'I',207-208,'L',210-214,

A/Experimental source: seed

R/Ren, J.; Wang, Y.; Dong, Y.; Stuart, D.I.

submitted to the Brookhaven Protein Data Bank, January 1994

A/Reference number: A52272; PDB:1MHC

A/Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-269

R/Husain, J.; Tickle, I.J.; Wood, S.P.

submitted to the Brookhaven Protein Data Bank, March 1994

A/Reference number: A52385; PDB:1MOM

A/Contents: annotation; X-ray crystallography, 2.16 angstroms, residues 24-86,'L',88-26

R/Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.

submitted to the Brookhaven Protein Data Bank, July 1994

A/Reference number: A67089; PDB:1MRH

A/Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-77,'R',79-132

C/Function: A/Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the

C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

C/Keywords: glycoprotein; glycosidase; hydrolase; lectin; seed; toxin

F/1-18/Domain: signal sequence #status predicted <SIG>

F/19-23/Domain: amino-terminal propeptide #status predicted <PRO>

F/24-269/Product: rRNA N-glycosidase alpha-momorcharin #status experimental <MAT>

F/270-286/Domain: rRNA N-glycosidase homology <RNG>

F/290-306/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F/310-326/Active site: Tyr, Gly, Arg #status predicted

F/330-346/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 65.7%; Score 802; DB 1; Length 286;
 Best Local Similarity 65.2%; Pred. No. 6.1e-50;
 Matches 161; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSGYGFISMLRKALPNERKLYDIPILRSGLPGSQRYALHLNVADETI 60
 |||||
 Db 24 DVSFRLSGATSSGYGFISMLRKALPNERKLYDIPILRSGLPGSQRYALHLNVADETI 60
 QY 61 SVADVTNYYIMGYRADGTSYFPNEASATEAAKYVFDAMRKYTLPPSGYERLQTAAGK 120
 |||||
 Db 84 TVADVTNYYIMGYRADGTSYFPNEASATEAAKYVFDAMRKYTLPPSGYERLQTAAGK 143
 QY 121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSAARAKYFIEQIIGKRVDTFL 180
 |||||
 Db 144 PREKIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSAARAKYFIEQIIGKRVDTFL 203
 QY 181 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAOQRVTITNVDAVGTSTNIAL 240
 |||||
 Db 204 PSIAITISLENSWGLSKQIOIASTNNGQFSPVLLINAOQRVTITNVDAVGTSTNIAL 263
 QY 241 LNENMMA 247
 |||||
 Db 264 LNENMMA 270

RESULT 6

S22494
 rRNA N-glycosidase (EC 3.2.2.22) alpha-luffin precursor - smooth loofah
 N/Alternate names: protein synthesis inhibitor; ribosome-inactivating protein luffin-A
 C/Species: Luffa cylindrica (smooth loofah)
 C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
 C/Accession: S22494; S26390; J06202; A32542
 R/Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
 Plant Mol. Biol. 18, 1199-1202, 1992
 A/Title: Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating pro
 A/Reference number: S22494; PMID:92288316; PMID:1600156
 A/Accession: S22494

RESULT 9

UC4235
rRNA N-glycosidase (EC 3.2.2.22) map30 precursor - balsam pear
N/Alternate names: anti-HIV 30K protein
C/Species: Momoricia charantia (balsam pear, bitter melon)
C/Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
A/Accession: J04235; S12869
R/Ref: Huang, S.; Huang, P.L.; Chen, H.C.; Huang, P.L.; Bourinbatar, A.; Huang, H.I.; Kun
Gene 161, 151-156, 1995
A/Title: Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter melon.
A/Reference number: J04235; PMID:95394347; PMID:7665070
A/Accession: J04235
A/Molecule type: DNA
A/Residues: 1-286 <LE>
A/Cross-references: UNIPROT:P24817
A/Experimental source: mature seeds
A/Note: The authors translated the codon TAC for residue 37 as Thr and ACT for residue 1
R/Ref: Huang, S.; Huang, P.L.; Nara, P.L.; Chen, H.C.; Kung, H.; Huang, P.; Huang, H.I.;
FEBS Lett. 272, 12-18, 1990
A/Title: MAP 30: a new inhibitor of HIV-1 infection and replication.
A/Reference number: S12869; PMID:91032105; PMID:1699801
A/Accession: S12869
A/Molecule type: protein
A/Residues: 24-36, 'r', 38-66, 'p' <LEW>
C/Comment: This plant protein has anti-HIV activity. It possesses antiviral action, anti
activation activities. It is capable of acting against multiple stages of the viral life
C/Comment: This protein has conserved unique residues Trp-213 and Met-277.
C/Genetic:
A/Genes: map30
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C/Keywords: antiviral; glycoprotein; glycosidase; hydrolase
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-286/Product: rRNA N-glycosidase (EC 3.2.2.22) map30 #status predicted <WAT>
F/27-264/Domain: rRNA N-glycosidase homology <RNG>
F/4/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/33,181,184/Active site: Tyr, Glu, Arg #status predicted

Query Match 57.8%; Score 706; DB 2; Length 286;
Best Local Similarity 61.2%; Pred. No. 7, 2e-52;
Matches 148; Conservative 31; Mismatches 61; Indels 2; Gaps 2;

QY 1 DVSFRLSGATSSSYGVFINLRKALPNEKLYDIPILRSLSGSRVALIHLTNVDEIT 60
DB 24 DVNFDLSTAYAKYTFIEBFRATLPFSHKVYDIPILYSTRISDRFILLNTSYAETI 83
QY 61 SVAIDVTNYINGYRAGDTSYFFNEASATEAKYVKDARKYTLPSGNYERLQTAACK 120
DB 84 SVAIDVTNYINGYRAGDTSYFFNEASATEAKYVKDARKYTLPSGNYERLQTAACK 141
QY 121 IRENIPGLPALDSATITLFFYNANSASALMVLIOSTSEARVKFIEQIGKRVDTFL 180
DB 142 IRENIPGLPALDSATITLFFYNANSASALMVLIOSTSEARVKFIEQIGKRVDTFL 201
QY 181 PSIAITISLEN-SWSALSKOIQIASTNNGQFESPVLINAOQRVTITNVDAVTSINATL 240
DB 202 PNIAITISLENQWALSQKQIFLQNOGQKFPNPVLLIKPTGERFQVNTVSDVYKGNIKLL 261
QY 241 LN 242
DB 262 LN 263

RESULT 10

JN0108
luffin-b - smooth loofah
C/Species: luffa cylindrica (smooth loofah)
C/Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C/Accession: JN0108
R/Ref: Islam, M.R.; Hidayat, H.; Punats, G.
Agric. Biol. Chem. 55, 229-238, 1991
A/Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from

A/Reference number: JN0108; PMID:91248488; PMID:1368666
A/Accession: JN0108
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-250 <ISL>
A/Cross-references: UNIPROT:P22851
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F/5-246/Domain: rRNA N-glycosidase homology <RNG>

Query Match 55.7%; Score 680; DB 2; Length 250;
Best Local Similarity 56.8%; Pred. No. 9, 1e-50;
Matches 142; Conservative 47; Mismatches 57; Indels 4; Gaps 3;

QY 1 DVSFRLSGATSSSYGVFINLRKALPNEKLYDIPILRSLSGSRVALIHLTNVDEIT 60
DB 2 NVFSLSGADSKSYKFFITLRLKALPSKRVSNIPILPSASGASRYTILMOLSNDAKAI 61
QY 61 SVAIDVTNYINGYRAGDTSYFFNEASATEAKYVKDARKYTLPSGNYERLQTAACK 120
DB 62 TWAIDVTNYINGYLVNSTYFANESDALKAQYFKGS-TLVITPSGNYERLQTAACK 120
QY 121 IRENIPGLPALDSATITLFFYNANSASALMVLIOSTSEARVKFIEQIGKRVDTFL 180
DB 121 IREKIPGLRALDSALTSIFHYDSTFAAFAFVILQTTAASRFKYEIGQITIERIPKNEY 180
QY 181 PSIAITISLEN-SWSALSKOIQIASTNNGQFESPVLINAOQRVTITNVDAVTS--NI 237
DB 181 PEPALISLENMWSLSKQIOLQTNNGAFRTPTVITDNKGQVETLGNLASKVKQIDVNS 240
QY 238 ALLINRNMA 247
DB 241 KLLNKNIA 250

RESULT 11

J04840
rRNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd

C/Species: Trichosanthes anguina (snake gourd)
C/Date: 15-Aug-1996 #sequence_revision 24-Oct-1997 #text_change 05-Dec-1997
C/Accession: J04840; J0701; J0677
R/Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.
Biomed. Sci. 3, 178-186, 1996
A/Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from
A/Reference number: J04840
A/Accession: J04840
A/Molecule type: protein
A/Residues: 1-132, 'S', 134-245 <CHO1>
A/Experimental source: seed
A/Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table
R/Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.
submitted to JIPID, August 1995
A/Description: Amino acid sequence of trichoanguina, a ribosomal-inactivating protein from

A/Reference number: J0677
A/Accession: J0701
A/Molecule type: protein

A/Residues: 1-50, 'L', 52-245 <CHO2>
C/Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C/Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed
F/4-242/Domain: rRNA N-glycosidase homology <RNG>
F/51,201/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/70,158,161/Active site: Tyr, Glu, Arg #status predicted
F/155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 54.6%; Score 666.5; DB 2; Length 245;
Best Local Similarity 57.0%; Pred. No. 1, 2e-48;
Matches 138; Conservative 34; Mismatches 67; Indels 3; Gaps 3;

QY 1 DVSFRLSGATSSSYGVFINLRKALPNEKLYDIPILRSLSGSRVALIHLTNVDEIT 60
DB 1 DVNFDLSTAYAKYTFIEBFRATLPFSHKVYDIPILYSTRISDRFILLNTSYAETI 83
QY 61 SVAIDVTNYINGYRAGDTSYFFNEASATEAKYVKDARKYTLPSGNYERLQTAACK 120

Db 61 IVAVDVTNVIYAVARADAVSYFFEDTPA-EAFKLIPA-GTKYVKLPSGNGYDLQSVGK 118

QY 121 IRENIPLGLPDLDSAITTLFFYNANSASASALMWLIOSTSEBARKYKIEQIGRVDKTEL 180

Db 119 ORDMELEGLPALSSAITTNWVVYDYOSTAALLATVLIOSTSEARARYKIEQVSSHSISNFY 178

QY 181 PSLAIISLNSMSALSATKOIQIAS-TNNGQESFPVVLINMNCQRVLTITNDACGYTSNIAL 229

Db 179 PNOAVIISLENKGAISAKOIQIANRGTGHGFENFVELYNDGTRFSVTHSAGVGNIKL 238

QY 240 LL 241

Db 239 LL 240

RESULT 12

ricin D precursor - castor bean
N:contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Ricinus communis (castor bean)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
A:Accession: A24041, S20513, A24614, A03374, A24010, A03374, S10903
R:Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A:Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A:Reference number: A24041, MUID:86067214; PMID:299712
A:Accession: A24041
A:Molecule type: DNA
A:Residues: 1-576 <HAL>
A:Cross-references: UNIPROT:P02879; GB:X03179; NID:G21082; PIDD:CAA26939.1; PID:G21083
R:Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A:Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene
A:Reference number: S20513, MUID:92163016; PMID:1371405
A:Accession: S20513
A:Molecule type: DNA
A:Residues: 1-576 <TR>
A:Cross-references: EMBL:X52908; NID:G21084; PIDD:CAA37095.1; PID:G21085
R:Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1985
A:Title: Nucleotide sequence of cloned cDNA coding for prepro-ricin.
A:Reference number: A24614, MUID:85179479; PMID:3838723
A:Accession: A24614
A:Molecule type: mRNA
A:Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAN>
A:Cross-references: GB:X02388; NID:G21077; PIDD:CAA26230.1; PID:G21078
R:Yoshitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A:Title: Isolation and sequences of peptic peptides, and the complete sequence of the cDNA
A:Reference number: A03372
A:Accession: A03372
A:Molecule type: protein
A:Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'V', 285-288, 290-302 <YOS>
A:Note: this paper cites the others in the series providing experimental details for the
R:Araki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A:Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan
A:Reference number: A24010
A:Accession: A24010
A:Molecule type: protein
A:Residues: 315-383, 'PS', 386-576 <ARA>
R:Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A:Title: Primary structure of Ala chain of ricin D.
A:Reference number: A03374
A:Accession: A03374
A:Molecule type: protein
A:Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 405
527, 'E', 529-564, 'V', 566, 'H', 567-570, 'LI', 573-574, 'P', <UN>
A:Note: this paper, one of a series, summarizes the experimental details for the determination
R:Ready, M.P.; Kim, Y.; Roberts, J.D.
Proteins 10, 270-278, 1991
A:Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of

A:Reference number: A48237; PMID:91352006; PMID:1861883
A:Contents: annotation; active site
R:Rutemder, E.; Robertus, J.D.
A:Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A:Reference number: A48238; PMID:91352005; PMID:1861882
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
R:Katzin, B.J.; Collins, E.G.; Robertus, J.D.
A:Title: Structure of ricin A-chain at 2.5 angstroms.
A:Reference number: A48239; PMID:91352004; PMID:1861881
A:Contents: annotation; X-ray crystallography, 2.5 angstroms
C:Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which C:Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subunit into the cell of the A chain; B chains are also responsible for cell agglutination (lectin C:Comment: This protein is cytotoxic and very poisonous to animals.
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F:1-35/Domain: signal sequence #status predicted <Sig>
F:36-302/Product: ricin D chain A #status experimental <ACH>
F:46-293/Domain: rRNA N-glycosidase homology <RNG>
F:315-576/Product: ricin D chain B #status experimental <BCB>
F:331-373, 374-414, 417-455, 462-497, 501-540, 543-576/Region: 40-residue repeats
F:445, 409, 449/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:415, 158, 243, 244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:212/Active site: Glu #status experimental
F:215/Active site: Arg #status predicted
F:239-318, 334-353, 377-394, 465-478, 504-521/Disulfide bonds: #status experimental
F:336, 349, 360/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status experimental
F:348, 369/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental

Query Match

Best Local Similarity 37.3%; Pred.No. 1.7e-27;
Matches 95; Conservative 60; Mismatches 82; Indels 18; Gaps 8

[illegible]

RESULT 13

agglutinin precursor - castor bean
N/Contents: rRNA-N-glycosidase (EC 3.2.2.22)
C/Species: Ricinus communis (castor bean)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A24261; A24210
J/Robert, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J. Biol. Chem. 260, 15682-15686, 1985
A/Title: The Primary Sequence of Ricinus communis agglutinin. Comparison with ricin.
A/Reference number: A24261; MUID:86059449; PMID:2299130
A/Accession: A24261
A/Molecule type: mRNA
A/Residues: 1-564 <ROB>
A/Cross-references: UNIPROT:P06750; GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g1697001
R/Ataki, T.; Yoshitaka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986

A>Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin
A/Reference number: A24210
A/Accession: A24210
A/Molecule type: protein
A/Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-
C/Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C/Superfamily: ricin; RNA N-glycosidase homology
C/Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F/1-24/Domain: signal sequence #status predicted <SIG>
F/25-230/Product: agglutinin chain A #status predicted <ACH>
F/33-281/Domain: RNA N-glycosidase homology <RMG>
F/303-564/Product: agglutinin chain B #status experimental <BCH>
F/319-361, 362-402, 405-443, 450-485, 489-528, 531-564/Region: 40-residue repeats
F/343-325/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/200,403/Active site: Glu, Arg #status predicted
F/282-306, 322-341, 365-382, 453-466, 492-509/Disulfide bonds: #status predicted
F/334,337,348/Binding site: N-acetylglucosamine (Asp, Gln, Asn) #status predicted
F/337,437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F/556,557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 32.5%; Score 396.5; DB 1; Length 564;
Best Local Similarity 37.3%; Pred. No. 1.9e-25;
Matches 95; Conservative 55; Mismatches 86; Indels 19; Gaps 9;

QY 2 VSRPLSGATSSSGVFIISNRKALPNERKL-YDIPLL-RSSLPGSGRYALIHITNVADE 58
DB 33 INFTADATVESYTNFIRAVRSHLTTGADVREHPVLPNRRGPIPSQRFILVELSNIAEL 92
QY 59 TISVAIDVTNVIYMGVAPGDTYFP--NEASATEAKVYFKDAMRKVTLPYSGNYERLQ 115
DB 93 SVTLADVTNAYVVGCAAGSAIRFHPDNOEDA-EALTHLFTDVQNSFTFAFGNNYRLR 151
QY 116 TAAKIRENIPGLPALDSAITTLFYNA-----NSAASALMWLIQSTSEARVYFIEQ 170
DB 152 QLGG-IKENIEELGPELDAISALYYSTGTGQPTLARSFVTCQIMISEARQYIEGE 210
QY 171 IGRKV-DKTFPLSLAISLNSWSALSQIQIASTNNQFESPVVLINQNRVITTNV 228
DB 211 MRRIRIRNRSAPDPSPVITLNSWGRSLTAIQ--ESNQGAFASPIQLRRNGSKFNV--Y 266

QY 229 DAGVTSNIALMLNR 243
DB 267 DVSILPIILMWIR 281

RESULT 14
C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
N/Contains: rRNA N-glycosidase (EC 3.2.2.22)
C/Species: Abrus precatorius (Indian licorice)
C/Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: C39761; S14471
R/Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A/Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A/Reference number: A39761; MOID:91201329; PMID:2016300
A/Accession: C39761
A/Molecule type: DNA
A/Residues: 1-251 <EVE>
A/Cross-references: UNIPROT:Q38760
R/Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A/Description: Direct molecular cloning of two distinct abrin A-chains.
A/Reference number: S14471
A/Accession: S14471
A/Molecule type: DNA
A/Residues: 'W', 1-251 <EY2>
A/Cross-references: EMBL:X54872; NID:916088; PIDN:CAA38654.1; PID:916089
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: duplication; glycosidase; hydrolase; lectin; toxin
F/1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F/7-246/Domain: rRNA N-glycosidase homology <RMG>

F/74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/164,167/Active site: Glu, Arg #status predicted

Query Match 28.8%; Score 352; DB 2; Length 251;
Best Local Similarity 38.6%; Pred. No. 3.4e-22;
Matches 95; Conservative 42; Mismatches 97; Indels 12; Gaps 8;

QY 2 VSRPLSGATSSSGVFIISNRKALPNERKLYDIPLLR--SSLPGSGRYALIHITNVADE 59
DB 5 IKSTGATSSQSKQPIEARRETL-RGGLHDPVLRDPTVERNRKYLITVELSNSRES 63
QY 60 ISVAIDVTNVIYMGVAPGDTYFPNEASATEAKVYFKDAMRKVTLPYSGNYERLQTAAG 119
DB 64 IEVGIDVTNAYVVGCAAGSAIRFHPDNPAS-ASTYLETGQR-YSLRFDQSYDGLERMAH 121
QY 120 KIRENIPGLPALDSAITTL--FYVANSASALMWLIQSTSEARVYFIEQIGK--RV 175
DB 122 QTRGQSLGLQALTHAISFLRSGASNDEKARFLIYIQWASBARVYISNRVGSIRF 181
QY 176 DKTFPLSLAISLNSWSALSQIQIASTNNQFESPVVLINQNRVITTNVDAVYTS 235
DB 182 GTFQPDPMWLSLNNWMDLSRGVQ--ESVQDTFPNAVTLRRVNPQVIVSLTHQSV-A 238
QY 236 NIALML 241
DB 239 VLALML 244

RESULT 15
S32431
abrin-d precursor - Indian licorice (fragment)
N/Contains: rRNA N-glycosidase (EC 3.2.2.22)
C/Species: Abrus precatorius (Indian licorice)
C/Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C/Accession: S32431; S34408
R/Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A/Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing.
A/Reference number: S32429; MOID:93132798; PMID:842113
A/Accession: S32431
A/Molecule type: mRNA
A/Residues: 1-528 <HUN>
A/Cross-references: UNIPROT:Q06076; GB:M98346
R/Hung, C.; Lee, M.; Lee, T.; Lin, J.
submitted to the EMBL Data Library, March 1993
A/Reference number: S34408
A/Accession: S34408
A/Molecule type: mRNA
A/Residues: 1169, 'C', 171-320, 'L', 322-528 <HUN>
A/Cross-references: GB:M98346
C/Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating
The A and B chains are linked by a single disulfide bond, which is essential for toxicity
C/Superfamily: ricin; rRNA N-glycosidase homology
C/Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F
F/1-251/Product: abrin-d chain A #status predicted <ACH>
F/7-246/Domain: rRNA N-glycosidase homology <RMG>
F/261-528/Product: abrin-d chain B #status predicted <BCH>
F/283-325, 326-366, 369-407, 414-449, 453-492, 495-528/Region: 40-residue repeats
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F/74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F/164,167/Active site: Glu, Arg #status predicted
F/200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/247-269, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
F/288,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F/500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 28.1%; Score 343; DB 2; Length 528;
Best Local Similarity 37.8%; Pred. No. 5.5e-21;
Matches 93; Conservative 43; Mismatches 98; Indels 12; Gaps 8;

QY 2 VSRPLSGATSSSGVFIISNRKALPNERKLYDIPLLR--SSLPGSGRYALIHITNVADE 59
DB 5 IKTTGATSSQSKQPIEARRLRLTG-GLIHDPVLRDPTVERNRKYLITVELSNSRES 63

QY 60 ISVAIDVTNYINGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPGSGNYERLQTAAG 119
Db 64 IEVGIDVTNAYVYVAYRAGSQSYFLRDPAS-ASTYLFPGTOR-YSLRFDGSYGDLERWMAH 121
QY 120 KIRENIPLGHPALDSAITTL--FYVANSASALMTLIQSTSEARYPFIEQIGK--RV 175
Db 122 QFREESISLGQALTTAHSFLRSGASNDEEKARTLIVIQASEARARYISNRVGSIRT 181
QY 176 DKTFPLSLAIIISLNSMSALSQIOIASTNNQFESPVVLLINQONQRTITNVDAGVTS 235
Db 182 GTRFQDPDPMLSLNNWNLSSGVQ--QSVQDTFPNNVILSSINRQPVVVDLSHPTV-A 238
QY 236 NIALLL 241
Db 239 VLALML 244

Search completed: April 12, 2005, 15:14:59
Job time : 26.3451 secs

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OM protein - protein search, using sw model

Run on: April 12, 2005, 15:14:19 ; Search time 81.5653 Seconds
(without alignments)
1005.370 Million cell updates/sec

Title: US-09-905-247a-8
Perfect score: 1221
Sequence: 1 DVAFRLSGATSSSYGVFISN.....VDAGVVTNIALLLNNRNA 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues
Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1221	100.0	247	9	US-09-792-793A-39
2	1221	100.0	247	15	US-10-375-209A-39
3	1214	99.4	289	11	US-09-805-247-1
4	1212	99.3	289	14	US-10-280-679B-4
5	1212	99.3	289	15	US-10-280-725B-4
6	1209	99.0	247	14	US-10-127-890-6
7	1209	99.0	247	17	US-10-127-890-6
8	1071	87.7	247	9	US-09-792-793A-34
9	1071	87.7	247	15	US-10-375-209A-34
10	802	65.7	263	14	US-10-127-890-7
11	802	65.7	263	17	US-10-127-890-7
12	724.5	59.3	248	14	US-10-127-890-5
13	724.5	59.3	248	17	US-10-127-890-5

14	709	58.1	263	14	US-10-127-890-4	Sequence 4, Appl
15	709	58.1	263	17	US-10-127-890-4	Sequence 4, Appl
16	421	34.5	267	14	US-10-282-935-1	Sequence 1, Appl
17	421	34.5	267	14	US-10-127-890-1	Sequence 1, Appl
18	421	34.5	267	15	US-10-440-796-1	Sequence 1, Appl
19	421	34.5	267	17	US-10-717-243-1	Sequence 1, Appl
20	421	34.5	267	14	US-10-083-336A-1	Sequence 1, Appl
21	342	28.0	198	14	US-10-083-336A-3	Sequence 3, Appl
22	342	28.0	198	14	US-10-083-336A-7	Sequence 7, Appl
23	342	28.0	198	14	US-10-083-336A-5	Sequence 5, Appl
24	342	28.0	198	14	US-10-083-336A-10	Sequence 10, Appl
25	337.5	27.6	185	14	US-10-083-336A-9	Sequence 9, Appl
26	336	27.5	188	14	US-10-083-336A-4	Sequence 4, Appl
27	336	27.5	188	14	US-10-083-336A-8	Sequence 8, Appl
28	336	27.5	189	14	US-10-083-336A-6	Sequence 6, Appl
29	336	27.5	190	14	US-10-083-336A-11	Sequence 11, Appl
30	330	27.0	251	14	US-10-282-935-3	Sequence 3, Appl
31	330	27.0	251	15	US-10-440-796-3	Sequence 3, Appl
32	326	26.7	252	9	US-09-347-064-2	Sequence 2, Appl
33	326	26.7	252	9	US-09-347-064-8	Sequence 8, Appl
34	323	26.5	251	14	US-10-127-890-99	Sequence 99, Appl
35	323	26.5	251	14	US-10-127-890-101	Sequence 101, Appl
36	323	26.5	251	14	US-10-127-890-107	Sequence 107, Appl
37	323	26.5	251	17	US-10-717-243-99	Sequence 99, Appl
38	323	26.5	251	17	US-10-717-243-101	Sequence 101, Appl
39	323	26.5	251	17	US-10-717-243-107	Sequence 107, Appl
40	322	26.4	251	14	US-10-127-890-110	Sequence 110, Appl
41	322	26.4	251	14	US-10-127-890-111	Sequence 111, Appl
42	322	26.4	251	17	US-10-717-243-110	Sequence 110, Appl
43	322	26.4	251	17	US-10-717-243-111	Sequence 111, Appl
44	321	26.3	251	9	US-09-765-527-247	Sequence 247, Appl
45	321	26.3	251	14	US-10-127-890-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-792-793A-39
Sequence 39, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosantheus kirilowii
US-09-792-793A-39

Query Match 100.0%; Score 1221; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.7e-112;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVAFRLSGATSSSYGVFISNLRKALNERKLYDIPILRSLPGSQRYALHLTNVADDT 60
DB 1 DVAFRLSGATSSSYGVFISNLRKALNERKLYDIPILRSLPGSQRYALHLTNVADDT 60
QY 61 SVADIDTNYIMYGRAGDTSYFENEASATEAKYVKDMARKYTLFYSQGYEYLTQTAAG 120
DB 61 SVADIDTNYIMYGRAGDTSYFENEASATEAKYVKDMARKYTLFYSQGYEYLTQTAAG 120
QY 121 IRENITLGLPAUDSAITTLFYYNANSASALMWLIQSTSEARARYKFIEOQIGKRVKTF 180
DB 121 IRENITLGLPAUDSAITTLFYYNANSASALMWLIQSTSEARARYKFIEOQIGKRVKTF 180

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QY      181 PSIAIISLSEWSALSQIOIASTNNQGFESPVLINQNRVTITNVDAVVTISNIALL 240
      |||
      181 PSIAIISLSEWSALSQIOIASTNNQGFESPVLINQNRVTITNVDAVVTISNIALL 240
QY      241 LNRNNMA 247
      |||
      241 LNRNNMA 247
Db      241 LNRNNMA 247

RESULT 2
US-10-375-209A-39
; Sequence 39, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Cogging, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Trichosanthes kirilowii
US-10-375-209A-39
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Query Match 100.0%; Score 1221; DB 15; Length 247;

Best Local Similarity 100.0%; Pred. No. 1.7e-112;

Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHITNVADETI 60
      |||
      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHITNVADETI 60
Db      61 SVAIDVTNVIYIMGRAGDTSYFENASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120
      |||
      61 SVAIDVTNVIYIMGRAGDTSYFENASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120
QY      121 IRENIPLGLPALDSATITLTFYNNANSASALMWLIQSTSEARVFTIQOIGKRVDTFL 180
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      121 IRENIPLGLPALDSATITLTFYNNANSASALMWLIQSTSEARVFTIQOIGKRVDTFL 180
Db      121 IRENIPLGLPALDSATITLTFYNNANSASALMWLIQSTSEARVFTIQOIGKRVDTFL 180
QY      181 PSIAIISLSEWSALSQIOIASTNNQGFESPVLINQNRVTITNVDAVVTISNIALL 240
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      181 PSIAIISLSEWSALSQIOIASTNNQGFESPVLINQNRVTITNVDAVVTISNIALL 240
QY      241 LNRNNMA 247
      |||
      241 LNRNNMA 247
Db      241 LNRNNMA 247

RESULT 3
US-09-905-247-1
; Sequence 1, Application US/09905247
; Publication No. US20040197853A1
; GENERAL INFORMATION:
; APPLICANT: KE, YI-BAO
; APPLICANT: NIE, HUI-LING
; TITLE OF INVENTION: Mutant Trichosanthin
; FILE REFERENCE: 04399/000615-USO
; CURRENT APPLICATION NUMBER: US/09/905,247
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: CN 00119553.0
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: CN 01103102.6
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 289
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; TYPE: PRT
; ORGANISM: Trichosanthes kirilowii M.
US-09-905-247-1
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Query Match 99.4%; Score 1214; DB 11; Length 289;

Best Local Similarity 99.6%; Pred. No. 1e-111;

Matches 246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHITNVADETI 60
      |||
      24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHITNVADETI 83
Db      61 SVAIDVTNVIYIMGRAGDTSYFENASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 120
      |||
      84 SVAIDVTNVIYIMGRAGDTSYFENASATEAKYVFKDAMRKVTLPSYGNVERLQTAAGK 143
QY      121 IRENIPLGLPALDSATITLTFYNNANSASALMWLIQSTSEARVFTIQOIGKRVDTFL 180
      |||
      144 IRENIPLGLPALDSATITLTFYNNANSASALMWLIQSTSEARVFTIQOIGKRVDTFL 203
Db      181 PSIAIISLSEWSALSQIOIASTNNQGFESPVLINQNRVTITNVDAVVTISNIALL 240
      |||
      204 PSIAIISLSEWSALSQIOIASTNNQGFESPVLINQNRVTITNVDAVVTISNIALL 263
QY      241 LNRNNMA 247
      |||
      264 LNRNNMA 270
Db      264 LNRNNMA 270
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RESULT 4

US-10-280-679B-4

; Sequence 4, Application US/10280679B

; Publication No. US20030150019A1

; GENERAL INFORMATION:

; APPLICANT: Large Scale Biology Corporation

; TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors

; FILE REFERENCE: LSBC-0109-US03

; CURRENT APPLICATION NUMBER: US/10/280,679B

; CURRENT FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 09/557,941

; PRIOR FILING DATE: 2000-04-24

; PRIOR APPLICATION NUMBER: 08/484,341

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 07/923,692

; PRIOR FILING DATE: 1992-07-31

; PRIOR APPLICATION NUMBER: 07/600,244

; PRIOR FILING DATE: 1990-10-22

; PRIOR APPLICATION NUMBER: 07/641,617

; PRIOR FILING DATE: 1991-01-16

; PRIOR APPLICATION NUMBER: 07/737,899

; PRIOR FILING DATE: 1991-07-26

; PRIOR APPLICATION NUMBER: 07/739,143

; PRIOR FILING DATE: 1991-08-01

; PRIOR APPLICATION NUMBER: 07/310,881

; PRIOR FILING DATE: 1989-02-17

; PRIOR APPLICATION NUMBER: 07/160,766

; PRIOR FILING DATE: 1988-02-26

; PRIOR APPLICATION NUMBER: 07/160,771

; PRIOR FILING DATE: 1988-02-26

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Chinese cucumber protein alpha-trichosanthin

US-10-280-679B-4

Query Match 99.3%; Score 1212; DB 14; Length 289;

Best Local Similarity 99.2%; Pred. No. 1.6e-111;

Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHITNVADETI 60
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Db 24 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPSCQRALHILTNVADETI 83
QY 61 SVAIDVTNYIMYKRGDTSYFFNEASATTAARYVFDAMRKVTLPYSGYERLQTAAGK 120
Db 84 SVAIDVTNYIMYKRGDTSYFFNEASATTAARYVFDAMRKVTLPYSGYERLQTAAGK 143
QY 121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARAKYFLEQIGKRVDTFL 180
Db 144 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARAKYFLEQIGKRVDTFL 203
QY 181 PSIAIISLNSWSALSKQIQIASTNNGOFESPVLINAQORVTITNVDAVGTSTNIAL 240
Db 204 PSIAIISLNSWSALSKQIQIASTNNGOFETPVLINAQORVITNVDAVGTSTNIAL 263
QY 241 LNRNMA 247
Db 264 LNRNMA 270

RESULT 5
US-10-280-725B-4
; Sequence 4, Application US/10280725B
; Publication No. US20040049025A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Recombinant Viral Nucleic Acids
; FILE REFERENCE: LSBC-0109-US02
; CURRENT APPLICATION NUMBER: US/10/280,725B
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/557,941
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 08/484,341
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600,244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641,617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737,899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739,143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310,881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160,766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160,771
; PRIOR FILING DATE: 1988-02-26
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Chinese cucumber
US-10-280-725B-4

Query Match 99.3%; Score 1212; DB 15; Length 289;
Best Local Similarity 99.2%; Pred. No. 1.6e-111;
Matches 245; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPSCQRALHILTNVADETI 60
Db 24 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPSCQRALHILTNVADETI 83
QY 61 SVAIDVTNYIMYKRGDTSYFFNEASATTAARYVFDAMRKVTLPYSGYERLQTAAGK 120
Db 84 SVAIDVTNYIMYKRGDTSYFFNEASATTAARYVFDAMRKVTLPYSGYERLQTAAGK 143
QY 121 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARAKYFLEQIGKRVDTFL 180

Db 144 IRENIPGLPALDSATITLTFYNNANSAASALMWLIQSTSEARAKYFLEQIGKRVDTFL 203
QY 181 PSIAIISLNSWSALSKQIQIASTNNGOFESPVLINAQORVTITNVDAVGTSTNIAL 240
Db 204 PSIAIISLNSWSALSKQIQIASTNNGOFETPVLINAQORVITNVDAVGTSTNIAL 263
QY 241 LNRNMA 247
Db 264 LNRNMA 270

RESULT 6
US-10-127-890-6
; Sequence 6, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnicka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-890-6

Query Match 99.0%; Score 1209; DB 14; Length 247;
Best Local Similarity 99.2%; Pred. No. 2.6e-111;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPSCQRALHILTNVADETI 60

DB 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLPGSQRYALHLTNVADETI 60
QY 61 SVAIDVTNVIYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 120
DB 61 SVAIDVTNVIYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 120
QY 121 IRENIPGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180
DB 121 IRENIPGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180
QY 181 PSIAIISLENSWSALSKOIQIASTNNGQFESPVLINAGNOVATITNDAGVVTSNIALL 240
DB 181 PSIAIISLENSWSALSKOIQIASTNNGQFESPVLINAGNOVATITNDAGVVTSNIALL 240
QY 241 LNRNNMA 247
DB 241 LNRNNMA 247

RESULT 7

US-10-717-243-6
Sequence 6, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 33,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-717-243-6

Query Match 99.0%; Score 1209; DB 17; Length 247;
Best Local Similarity 99.2%; Pred. No. 2,6e-11;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLPGSQRYALHLTNVADETI 60
DB 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLPGSQRYALHLTNVADETI 60
QY 61 SVAIDVTNVIYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 120
DB 61 SVAIDVTNVIYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 120
QY 121 IRENIPGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180
DB 121 IRENIPGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180
QY 181 PSIAIISLENSWSALSKOIQIASTNNGQFESPVLINAGNOVATITNDAGVVTSNIALL 240
DB 181 PSIAIISLENSWSALSKOIQIASTNNGQFESPVLINAGNOVATITNDAGVVTSNIALL 240
QY 241 LNRNNMA 247
DB 241 LNRNNMA 247

RESULT 8

US-09-792-793A-34
Sequence 34, Application US/09792793A
Patent No. US20020168370A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
Coghins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
CURRENT APPLICATION NUMBER: US/09/792,793A
FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 34
LENGTH: 247
TYPE: PRT
ORGANISM: Bryonia dioica
US-09-792-793A-34

Query Match 87.7%; Score 1071; DB 9; Length 247;
Best Local Similarity 86.2%; Pred. No. 1.2e-97;
Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLPGSQRYALHLTNVADETI 60
DB 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLPGSQRYALHLTNVADETI 60
QY 61 SVAIDVTNVIYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 120
DB 61 SVAIDVTNVIYIMGYRAGDTSYFFNEASATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 120
QY 121 IRENIPGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180
DB 121 IRENIPGLPALDSATITLTFYNNANSASALMWLIQSTSEARARYFIEQOIGKRVDTFL 180
QY 181 PSIAIISLENSWSALSKOIQIASTNNGQFESPVLINAGNOVATITNDAGVVTSNIALL 240
DB 181 PSIAIISLENSWSALSKOIQIASTNNGQFESPVLINAGNOVATITNDAGVVTSNIALL 240
QY 241 LNRNNMA 247
DB 241 LNRNNMA 247

RESULT 9
US-10-375-209A-34
Sequence 34, Application US/10375209A
Publication No. US20030215421A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 25020-601E
CURRENT APPLICATION NUMBER: US/10/375, 209A
CURRENT FILING DATE: 2003-02-24
NUMBER OF SEQ. ID NOS: 93
SOFTWARE: Patent In Ver. 2.0
SEQ. ID NO: 34
LENGTH: 247
TYPE: PRT
ORGANISM: Bryonia dioica
US-10-375-209A-34

Query Match 87.7%; Score 1071; DB 15; Length 247;
Best Local Similarity 86.2%; Pred. No. 1.2e-97;
Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 DVSEFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHITNYADETI 60
1 DVSEFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHITNYADETI 60
DB 1 DVSEFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHITNYADETI 60
QY 61 SVADVTNVIYIMGYRAGDTSYFENEASATEAKVFDARKVTLTPYSGYVERLOTAAGK 120
61 SVADVTNVIYIMGYRAGDTSYFENEASATEAKVFDARKVTLTPYSGYVERLOTAAGK 120
DB 61 SVADVTNVIYIMGYRAGDTSYFENEASATEAKVFDARKVTLTPYSGYVERLOTAAGK 120
QY 121 IRENIPGLPALDSATITLTFYVANSASALMWLIQSTSEARVYKIEQOIGKRVDTFL 180
121 IRENIPGLPALDSATITLTFYVANSASALMWLIQSTSEARVYKIEQOIGKRVDTFL 180
DB 121 IRENIPGLPALDSATITLTFYVANSASALMWLIQSTSEARVYKIEQOIGKRVDTFL 180
QY 181 PSLATISLENSMGSLSKQIOIASTNNGQFSPVVLINAGNORVITTNVAGVTSNIAL 240
181 PSLATISLENSMGSLSKQIOIASTNNGQFSPVVLINAGNORVITTNVAGVTSNIAL 240
DB 181 PSLATISLENSMGSLSKQIOIASTNNGQFSPVVLINAGNORVITTNVAGVTSNIAL 240
QY 241 LNENMNA 247
241 LNENMNA 247
DB 241 LNENMNA 247

RESULT 10
US-10-127-890-7
Sequence 7, Application US/10127890
Publication No. US2003016196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127, 890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8869
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-127-890-7

Query Match 65.7%; Score 802; DB 14; Length 263;
Best Local Similarity 65.2%; Pred. No. 6.1e-71;
Matches 161; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

QY 1 DVSEFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHITNYADETI 60
1 DVSEFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHITNYADETI 60
DB 1 DVSEFRLSGATSSSYGVFISLURKALPNERKLYDIPILRSSLPQSORYALHITNYADETI 60
QY 61 SVADVTNVIYIMGYRAGDTSYFENEASATEAKVFDARKVTLTPYSGYVERLOTAAGK 120
61 SVADVTNVIYIMGYRAGDTSYFENEASATEAKVFDARKVTLTPYSGYVERLOTAAGK 120
DB 61 SVADVTNVIYIMGYRAGDTSYFENEASATEAKVFDARKVTLTPYSGYVERLOTAAGK 120
QY 121 IRENIPGLPALDSATITLTFYVANSASALMWLIQSTSEARVYKIEQOIGKRVDTFL 180
121 IRENIPGLPALDSATITLTFYVANSASALMWLIQSTSEARVYKIEQOIGKRVDTFL 180
DB 121 IRENIPGLPALDSATITLTFYVANSASALMWLIQSTSEARVYKIEQOIGKRVDTFL 180
QY 181 PSLATISLENSMGSLSKQIOIASTNNGQFSPVVLINAGNORVITTNVAGVTSNIAL 240
181 PSLATISLENSMGSLSKQIOIASTNNGQFSPVVLINAGNORVITTNVAGVTSNIAL 240
DB 181 PSLATISLENSMGSLSKQIOIASTNNGQFSPVVLINAGNORVITTNVAGVTSNIAL 240
QY 241 LNENMNA 247
241 LNENMNA 247
DB 241 LNENMNA 247

RESULT 11
US-10-717-243-7
Sequence 7, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

RESULT 13

US-10-717-243-5
Sequence 5, Application US/10717243
Publication No. US20050054635A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/717,243

FILING DATE: 18-Nov-2003

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-717-243-5

Query Match 59.3%; Score 724.5; DB 17; Length 248;

Best Local Similarity 59.0%; Pred. No. 2,7e-63;

Matches 147; Conservative 49; Mismatches 50; Indels 3; Gaps 3;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

DB 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

QY 61 SVADIDVTNVYIMGRAGDTSYFPEAGATEAKVFDARAKYTLPEYSGNYERLQTAAGK 120

DB 61 TVAVDSQIYIMGYLVNSTSYFPEAGATEAKVFDARAKYTLPEYSGNYERLQTAAGK 119

QY 121 IRENIPLGLPALDSAITTLFFYNNASASALMWLIQSTSAARYKFLIQIGKRVDTFL 180

DB 120 IRENIPLGLPALDSAITTLFFYNNASASALMWLIQSTSAARYKFLIQIGKRVDTFL 179

QY 181 PSIAIISLENS-WSALSQIOIASTNNNGOFESPVLLINQNRVITTNVAGVTSNIAL 239

DB 180 PSIAIISLENS-WSALSQIOIASTNNNGOFESPVLLINQNRVITTNVAGVTSNIAL 239

QY 240 LNN-RNNMA 247

DB 240 LNN-RNNMA 248

RESULT 14

US-10-127-890-4

Sequence 4, Application US/10127890

Publication No. US20030166196A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-127-890-4

Query Match 58.1%; Score 709; DB 14; Length 263;

Best Local Similarity 61.6%; Pred. No. 1e-61;

Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

DB 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSLSPGSQRYALHLTNVADDTI 60

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2005, 14:56:17 ; Search time 106.91 Seconds

(without alignments)
1183.080 Million cell updates/sec

Title: US-09-905-247A-8

Perfect score: 1221

Sequence: 1 DVSGFRLSGATSSSYGVFISN.....VDAGVTSNIALLNENMA 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1221	100.0	289	1	RIP1 TRIKI
2	1218	99.8	289	1	RIP1 TRIKI
3	1217	99.7	289	2	Q94SV8
4	1207	98.9	289	2	Q94K64
5	1195	97.9	289	2	Q41216
6	1194	97.8	289	2	Q6B8Q4
7	1187	97.2	289	1	RIPS TRIKI
8	1162	95.2	270	2	Q91RE3
9	1162	95.2	270	2	Q41611
10	1158	94.8	270	2	Q6PRG5
11	1071	87.7	290	1	RIP1 BRYDI
12	802	65.7	286	1	RIP1 MOMCH
13	754	61.8	277	1	RIP1 LURCY
14	728.5	59.7	278	2	Q00980
15	711	58.2	264	2	Q684D5
16	711	58.2	264	2	Q684D5
17	709	58.1	286	1	RIP3 MOMCH
18	691.5	56.6	286	1	RIP2 MOMBA
19	680	55.7	250	1	RIP1 CUCFI
20	644.5	52.8	294	1	RIP1 TRIAN
21	535	43.8	282	1	RIP2 BRYDI
22	476.5	39.0	136	2	Q8SAD7
23	425.5	34.8	561	2	Q8G1T2
24	425	34.8	541	2	Q41174
25	421	34.5	576	1	RICI RICCO
26	420.5	34.4	563	1	NIGI SAMNI
27	419.5	34.4	563	2	Q94S52
28	417.5	34.2	275	2	Q04367
29	415.5	34.0	136	2	Q8H1Y4
30	412.5	33.8	580	2	Q8SAG0
31					Q94BW4

ALIGNMENTS

32	408.5	33.5	580	2	Q94BM3	Q94BW3 cinamomum
33	407.5	33.4	275	2	Q84LJ1	Q84LJ1 gnostemma
34	405.5	33.2	581	2	Q94BW5	Q94BW5 cinamomum
35	404.5	33.1	564	2	Q94VR2	Q94VR2 sambucus eb
36	403.5	33.0	277	2	Q8GV09	Q8GV09 gnostemma
37	403.5	33.0	549	2	Q9FV22	Q9FV22 cinamomum
38	401.5	32.9	277	2	Q84UR1	Q84UR1 gnostemma
39	400.5	32.8	277	2	Q8GV11	Q8GV11 gnostemma
40	396.5	32.5	564	1	AGGL RICCO	P06750 ricinus com
41	395.5	32.4	277	2	Q8H1Y5	Q8H1Y5 gnostemma
42	393.5	32.2	136	2	Q84LJ0	Q84LJ0 cucurbita m
43	392.5	32.1	136	2	Q84LJ9	Q84LJ9 cucurbita m
44	388.5	31.8	277	2	Q8GV10	Q8GV10 gnostemma
45	384.5	31.5	136	2	Q8S2R5	Q8S2R5 cucurbita m

RESULT 1

AC	RIP1 TRIKI	STANDARD;	PRT;	289 AA.
ID	P09889;			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DE	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Ribosome-inactivating protein alpha-trichosanthin precursor			
DE	(EC 3.2.2.22) (RNA N-glycosidase) (Alpha-TCS).			
OS	Trichosanthes kirilowii (Mongolian snake-gourd).			
OC	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid I; Cucurbitales; Cucurbitaceae; Trichosanthes.			
OX	NCBI_TaxID=3677;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Maximowicz;			
RX	MEDLINE=91153657; PubMed=1999291; DOI=10.1016/0378-1119(91)90061-F;			
RA	Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;			
RT	"Cloning of trichosanthin cDNA and its expression in Escherichia			
RT	coli.";			
RL	Gene 97:267-272(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Maximowicz; TISSUE=leaf;			
RX	MEDLINE=90256790; PubMed=2341400;			
RA	Chow T., Feldman R.A., Lovett M., Piatek M.;			
RT	"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a			
RT	type I ribosome-inactivating protein.";			
RL	J. Biol. Chem. 265:8670-8674(1990).			
RN	[3]			
RP	SEQUENCE OF 24-270.			
RC	STRAIN=Maximowicz; TISSUE=tuberous root;			
RX	MEDLINE=90256789; PubMed=2341399;			
RA	Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,			
RA	Wu P., Hwang K., Piatek M.;			
RT	"Primary amino acid sequence of alpha-trichosanthin and molecular			
RT	models for abrin A-chain and alpha-trichosanthin.";			
RL	J. Biol. Chem. 265:8665-8669(1990).			
RN	[4]			
RP	TISSUE=tuberous root;			
RC	Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,			
RA	Tian G.Y., Ni C.Z.;			
RT	"Scientific evaluation of Tian Hua Fen (THF): history, chemistry and			
RT	application.";			
RL	Pure Appl. Chem. 58:789-798(1996).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).			
RX	MEDLINE=94344957; PubMed=806085;			
RA	Zhou F., Fu Z., Chen M., Lin Y., Pan K.;			
RT	"Structure of trichosanthin at 1.88-A resolution.";			
RL	Proteins 19:4-13(1994).			
RN	[6]			

RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RA MEDLINE=95344383; PubMed=7619070;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.,
 RT "Studies on crystal structures, active-centre geometry and
 RT deprotonating mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J 309:285-298(1995).
 CC -1- FUNCTION: Trichosanthin is an abortion-inducing protein. It is
 CC capable of inhibiting HIV-1 infection and replication. It
 CC inactivates eukaryotic 60S ribosomal subunits.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M34858; AAA34207.1; -;
 DR EMBL; J05434; AAA34206.1; -;
 DR PIR; J70566; RLTZT.
 DR PDB; 1GIS; X-ray; A=23-270.
 DR PDB; 1GIU; X-ray; A=24-270.
 DR PDB; 1J4G; X-ray; A/B/C/D=23-270.
 DR PDB; 1MRJ; X-ray; @=24-270.
 DR PDB; 1MRK; X-ray; @=24-270.
 DR PDB; 1NLI; X-ray; A=23-270.
 DR PDB; 1QD2; X-ray; A=24-270.
 DR PDB; 1TCS; X-ray; @=24-270.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW 3D-structure; Antiviral; Direct protein sequencing; Hydrolase;
 KW Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT CHAIN 1 23
 FT SIGNAL 24 270
 FT PROPEP 271 289
 FT ACT_SITE 183 183
 FT CONFLICT 57 60
 FT CONFLICT 82 84
 FT CONFLICT 87 87
 FT CONFLICT 92 92
 FT CONFLICT 143 144
 FT CONFLICT 196 196
 FT CONFLICT 215 216
 FT CONFLICT 231 231
 FT CONFLICT 234 234
 FT CONFLICT 246 266
 FT CONFLICT 247 247
 FT STRAND 25 28
 FT TURN 30 31
 FT HELIX 34 46
 FT TURN 47 47
 FT STRAND 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 69
 FT STRAND 70 76
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 89 92
 FT STRAND 93 99
 FT TURN 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT TURN 115 117
 FT TURN 120 121

Removed in mature form.
 By similarity.
 IPR -> IPR1 (in Ref. 4).
 Missing (in Ref. 4).
 I -> L (in Ref. 4).
 V -> VDAIIPRNV (in Ref. 4).
 KI -> GL (in Ref. 4).
 K -> S (in Ref. 4).
 WS -> LML (in Ref. 4).
 Q -> T (in Ref. 4).
 S -> T (in Ref. 2).
 Missing (in Ref. 4).
 T -> W (in Ref. 2).
 Ribosome-inactivating protein alpha-trichosanthin.

FT STRAND 124 127
 FT HELIX 134 141
 FT TURN 142 142
 FT HELIX 145 147
 FT STRAND 150 150
 FT HELIX 152 163
 FT TURN 164 165
 FT HELIX 167 180
 FT TURN 181 181
 FT HELIX 182 186
 FT STRAND 187 187
 FT HELIX 188 195
 FT TURN 196 196
 FT STRAND 202 202
 FT HELIX 206 226
 FT TURN 227 230
 FT STRAND 231 239
 FT TURN 241 242
 FT STRAND 245 250
 FT TURN 251 252
 FT HELIX 254 258
 FT TURN 259 259
 FT STRAND 260 260
 FT STRAND 263 263
 FT TURN 266 268
 SQ SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;
 Query Match 100.0%; Score 1221; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 4,7e-92;
 Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQGRVALIHLTNYADETI 60
 DB 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQGRVALIHLTNYADETI 83
 QY 61 SVAIDVTNYIMGYAGSTSYFENASATBAKYFKDAMKVTLPYSGNVERLOTAGK 120
 DB 84 SVAIDVTNYIMGYAGSTSYFENASATBAKYFKDAMKVTLPYSGNVERLOTAGK 143
 QY 121 IRENIPGLPALDSAITTLFYNNASASALMWLIQSTSEARYFYEQOIGKVDKTEL 180
 DB 144 IRENIPGLPALDSAITTLFYNNASASALMWLIQSTSEARYFYEQOIGKVDKTEL 203
 QY 181 PSLAIISSNSWSALSKQIQIASTNNGQFESPVLINQONRVITTNVDAVVTSNIAL 240
 DB 204 PSLAIISSNSWSALSKQIQIASTNNGQFESPVLINQONRVITTNVDAVVTSNIAL 263
 QY 241 LNRNMA 247
 DB 264 LNRNMA 270
 RESULT 2
 Q84SV8 PRELIMINARY; PRT; 289 AA.
 AC Q84SV8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Trichosanthin.
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.

FT	SIGNAL	1	23	Potential.
FT	CHAIN	24	270	Trichosanthin.
SD	SEQUENCE	289 AA;	31706 MM; AAD5602549CA5657 CRC64;	
	Query Match	99.7%;	Score 1217; DB 2;	Length 289;
	Best Local Similarity	99.2%;	Pred. No. 1e-91;	
	Matches 245;	Conservative 2;	Mismatches 0;	Indels 0; Gaps 0
OY	1 DVSEFRLSGATSSSYGVFIISNRKALPNERKLYDIPILRSSLPGSGRYALIHLTNYADETI	60		
DB	24 DVSEFRLSGATSSSYGVFIISNRKALPNERKLYDIPILRSSLPGSGRYALIHLTNYADETI	83		
OY	61 SVAIDVTNVMYIMGRAGDTSYFFNEASATEAKVYFKDMARKVTLPYGNTVERLLOTAAGK	120		
DB	84 SVAIDVTNVMYIMGRAGDTSYFFNEASATEAKVYFKDSMKRITLPYGSNERLLOTAAGK	143		
OY	121 IRENIPLGLPDLDAITTLTFYYNNNSASALMWLIQSTSEARARYFTIOQIGKRDKEFL	180		
DB	144 IRENIPLGLPDLDAITTLTFYYNNNSASALMWLIQSTSEARARYFTIOQIGKRDKEFL	203		
OY	181 PSLAIISLENSWSALSKOIQASTNNQGFEPSPVLLINONORVTTINDAGVTSINALL	240		
DB	204 PSLAIISLENSWSALSKOIQASTNNQGFEPSPVLLINONORVTTINDAGVTSINALL	263		
OY	241 LNRNNMA 247			
DB	264 LNRNNMA 270			
	RESULT 4			
	Q41216 PRELIMINARY; PRT; 289 AA.			
ID	Q41216			
AC	Q41216:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Trichosanthin.			
GN	Name=trichosanthin; Synonyms=TCS;			
OS	Trichosanthes kirilowii (Mongolian snake-gourd).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosoids I; Cucurbitales; Cucurbitaceae; Trichosanthes.			
OX	NCBI_TaxID=3677;			
RN	[1]			
RP	SEQUENCE FROM N.A..			
FX	MEDLINE=94271613; PubMed=8003348;			
RA	Zheng H., Wang B., Shaw P., Yeung H.;			
RT	"Cloning and DNA sequencing of the gene encoding trichosanthin.";			
RL	I Chuan Heunh Pac 21:42-51(1994).			
CC	-I CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one			
CC	specific adenosine on the 28S rRNA.			
CC	-I SIMILARITY: Belongs to the ribosome-inactivating protein family.			
DR	EMBL; J70176; AB331048.1; -.			
DR	PIR; JC5032; JC5032.			
DR	HSSP; P09989; 1d4G.			
DR	GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.			
DR	InterPro; IPRO01574; RIP.			
DR	Pfam; PF00161; RIP; 1.			
DR	PRINTS; PR00396; SHGARICIN.			
DR	PROSITE; PS00275; SHIGA_RICIN; 1.			
KW	Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.			
SD	SEQUENCE 289 AA; 31650 MM; 266AC14D8BCA175 CRC64;			
	Query Match	98.9%;	Score 1207; DB 2;	Length 289;
	Best Local Similarity	98.4%;	Pred. No. 6.6e-91;	
	Matches 243;	Conservative 4;	Mismatches 0;	Indels 0; Gaps 0
OY	1 DVSEFRLSGATSSSYGVFIISNRKALPNERKLYDIPILRSSLPGSGRYALIHLTNYADETI	60		
DB	24 DVSEFRLSGATSSSYGVFIISNRKALPNERKLYDIPILRSSLPGSGRYALIHLTNYADETI	83		
OY	61 SVAIDVTNVMYIMGRAGDTSYFFNEASATEAKVYFKDMARKVTLPYGNTVERLLOTAAGK	120		
DB	84 SVAIDVTNVMYIMGRAGDTSYFFNEASATEAKVYFKDSMKRITLPYGSNERLLOTAAGK	143		
OY	121 IRENIPLGLPDLDAITTLTFYYNNNSASALMWLIQSTSEARARYFTIOQIGKRDKEFL	180		
DB	144 IRENIPLGLPDLDAITTLTFYYNNNSASALMWLIQSTSEARARYFTIOQIGKRDKEFL	203		
OY	181 PSLAIISLENSWSALSKOIQASTNNQGFEPSPVLLINONORVTTINDAGVTSINALL	240		
DB	204 PSLAIISLENSWSALSKOIQASTNNQGFEPSPVLLINONORVTTINDAGVTSINALL	263		
OY	241 LNRNNMA 247			
DB	264 LNRNNMA 270			

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Db      84  SVAIDVTSYIMGADTSYFENFNEASATEAKYFKDARKKTLTPYSGYERLQTPAAK 143
      121  IRENIPILGIPALDSATITLTPYVANSASALMWLIQSTSPAAKYKFEQOIGKRVKTF 180
      144  IRENIPILGIPALDSATITLTPYVANSASALMWLIQSTSPAAKYKFEQOIGKRVKTF 203
Qy      181  PSIAITISLENSWSALSKQIOIASTNNQGFESPVVLINAGQRTITNVDAVTSNIAL 240
      204  PSIAITISLENSWSALSKQIOIASTNNQGFETPVVLINAGQRTITNVDAVTSNIAL 263
Qy      241  LNRNNMA 247
      264  LNRNDMA 270
Db

RESULT 5
06B04
ID      06B04      PRELIMINARY,      PRT,      247 AA.
AC      06B04;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Trichosanthin (Fragment).
GN      Name=TrCS;
OS      Trichosanthes kirilowii (Mongolian snake-gourd).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX      NCBI_TaxID=3677;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      M1 S.-L., Wang Y., Li Y.-Y., Chen Z.-L., An C.-C.;
RA      "Trichosanthes kirilowii trichosanthin (TCS) mature peptide gene.";
RL      Submitted (JUN-2004) to the EMBL/GenBank/DDAJ databases.
CC      -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC      EMBL; AY669811; AAT91090.1; -.
DR      GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
DR      GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR      InterPro; IPR001574; RIF.
DR      Pfam; PF00161; RIF; 1.
DR      PRINTS; PR00396; SHIGARICIN.
DR      PROSITE; PS00275; SHIGA_RICIN; 1.
KW      Hydrolyase; plant defense; Protein synthesis inhibitor; Toxin.
FT      CHAIN 1 1
FT      NON_TER <1 247 trichosanthin.
FT      TER 247
SQ      SEQUENCE 247 AA; 27172 MW; BCBA762884F9CCE CRC64;

Query Match 97.9%; Score 1195; DB 2; Length 247;
Best Local Similarity 97.6%; Pred. No. 5.2e-90;
Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSGRYALHILTNVADDTI 60
      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSGRYALHILTNVADDTI 60
Db      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSGRYALHILTNVADDTI 60
Qy      61  SVAIDVTNNYIMGIRAGDTSYFENFNEASATEAKYFKDARKKTLTPYSGYERLQTPAAK 120
      61  SVAIDVTNNYIMGIRAGDTSYFENFNEASATEAKYFKDARKKTLTPYSGYERLQTPAAK 120
Db      61  SVAIDVTNNYIMGIRAGDTSYFENFNEASATEAKYFKDARKKTLTPYSGYERLQTPAAK 120
Qy      121  IRENIPILGIPALDSATITLTPYVANSASALMWLIQSTSPAAKYKFEQOIGKRVKTF 180
      121  IRENIPILGIPALDSATITLTPYVANSASALMWLIQSTSPAAKYKFEQOIGKRVKTF 180
Db      121  IRENIPILGIPALDSATITLTPYVANSASALMWLIQSTSPAAKYKFEQOIGKRVKTF 180
Qy      181  PSIAITISLENSWSALSKQIOIASTNNQGFESPVVLINAGQRTITNVDAVTSNIAL 240
      181  PSIAITISLENSWSALSKQIOIASTNNQGFETPVVLINAGQRTITNVDAVTSNIAL 240
Db      181  PSIAITISLENSWSALSKQIOIASTNNQGFETPVVLINAGQRTITNVDAVTSNIAL 240
Qy      241  LNRNNMA 247
      241  LNRNNMA 247

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Db      241  LNRNNMA 247
      241  LNRNNMA 247
Db

RESULT 6
RIPS TRIKI
ID      RIPS TRIKI      STANDARD;      PRT,      289 AA.
AC      P24478;
DT      01-MAR-1992 (Rel. 21, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Ribosome-inactivating protein karasurin precursor (EC 3.2.2.22) (rRNA
DE      N-glycosidase).
OS      Trichosanthes kirilowii (Mongolian snake-gourd).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX      NCBI_TaxID=3677;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      TISSUE=Root tuber;
RC      MEDLINE=97356562; PubMed=9212998;
RX      Mizukami H., Iida K., Kondo T., Ogihara Y.;
RT      "Cloning and bacterial expression of a gene encoding ribosome-
RT      inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
RT      kirilowii var. 'japonica.'
RL      Biol. Pharm. Bull. 20:711-713 (1997).
RN      [2]
RP      SEQUENCE OF 24-270.
RX      MEDLINE=92005921; PubMed=1914000;
RA      Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
RT      "The complete amino acid sequence of an abortifacient protein,
RT      karasurin."
RL      Chem. Pharm. Bull. 39:1244-1249 (1991).
CC      -1- FUNCTION: Abortion-inducing protein. It inactivates eukaryotic 60S
CC      ribosomal subunits.
CC      -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC      Type 1 RIF subfamily.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB000666; BAA21786.1; -.
DR      PIR; JC5606; JC5606.
DR      PIR; JU0393; JU0393.
DR      HSSP; P09989; 1MRJ.
DR      InterPro; IPR001574; RIF.
DR      Pfam; PF00161; RIF; 1.
DR      PRINTS; PR00396; SHIGARICIN.
DR      PROSITE; PS00275; SHIGA_RICIN; 1.
KW      Antiviral; Direct protein sequencing; Hydrolase; Plant defense;
KW      Protein synthesis inhibitor; Signal; Toxin.
FT      SIGNAL 1 21
FT      CHAIN 22 270
FT      FT
FT      CHAIN 24 270
FT      FT
FT      PROPEP 271 289
FT      ACT_SITE 183 183
FT      SEQUENCE 289 AA; 31704 MW; 883D3E3242887B26 CRC64;

Query Match 97.8%; Score 1194; DB 1; Length 289;
Best Local Similarity 97.6%; Pred. No. 7.7e-90;
Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSGRYALHILTNVADDTI 60
      1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSGRYALHILTNVADDTI 60

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Db      24 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPSCQRVALIHLTNVADETI 83
Qy      61 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKVTLTPYSGNYERLQTPAGK 120
Db      84 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKVTLTPYSGNYERLQTPAGK 143
Qy      121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARAKYFIEQOIGKRVDTFL 180
Db      144 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARAKYFIEQOIGKRVDTFL 203
Qy      181 PSIAIISLNSWSALSQIOIASTNNGQFESPVLINAOQRVTITNVDAVTSNIAL 240
Db      204 PSIAIISLNSWSALSQIOIASTNNGQFETPVLLINAOQRVTITNVDAVTSNIAL 263
Qy      241 LNRNNMA 247
Db      264 LNRNNMA 270

RESULT 7
Q9LRE3 PRELIMINARY; PRT; 247 AA.
ID 09LRE3
AC 09LRE3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Trichobakin (Fragment).
GN Name=TBK;
OS Trichosanthes sp. Bac Kan 8-98.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside 1; Cucurbitales; Cucurbitaceae; Trichosanthes.
NCBI_TaxID=118182;
RN [1]
RA SEQUENCE FROM N.A.
RX MEDLINE=21476888; PubMed=11592913;
RA Van Chi P., Quoc Truong H., Thuy Ha N., Chung W.I., Binh L.T.;
RT "Characterization of trichobakin, a type I ribosome-inactivating
RT protein from Trichosanthes sp. Bac Kan 8-98."
RL Biotechnol. Appl. Biochem. 34:85-92(2001).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL: AB039324; BAA92530.1; -.
DR HSSP: P09989; 1U4G.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO: GO:0009405; P:patogenesis; IEA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 1
FT TER 247
SQ SEQUENCE 247 AA; 27199 MW; 89811AC32892F03F CRC64;

Query Match 97.2%; Score 1187; DB 2; Length 247;
Best local Similarity 97.2%; Pred. No. 2.4e-89;
Matches 240; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPSCQRVALIHLTNVADETI 60
Db      1 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPSCQRVALIHLTNVADETI 60
Qy      61 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKVTLTPYSGNYERLQTPAGK 120
Db      61 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKVTLTPYSGNYERLQTPAGK 120
Qy      121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARAKYFIEQOIGKRVDTFL 180
Db      121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARAKYFIEQOIGKRVDTFL 180

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Db      121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARAKYFIEQOIGKRVDTFL 180
Qy      181 PSIAIISLNSWSALSQIOIASTNNGQFESPVLINAOQRVTITNVDAVTSNIAL 240
Db      181 PSIAIISLNSWSALSQIOIASTNNGQFETPVLLINAOQRVTITNVDAVTSNIAL 240
Qy      241 LNRNNMA 247
Db      241 LNRNNMA 247

RESULT 8
Q41611 PRELIMINARY; PRT; 270 AA.
ID 041611
AC 041611;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Trichosanthes kirilowii (Mongolian snake-gourd).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside 1; Cucurbitales; Cucurbitaceae; Trichosanthes.
NCBI_TaxID=3677;
RN [1]
RA SEQUENCE FROM N.A.
RA Bao Y., Chu R., Han J., Zhang H., Pan N., Gu X., Chen Z.;
RT "Cloning and sequencing of trichosanthin gene and its expression in
RT Escherichia coli and tobacco plant."
RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 36:669-676(0).
RN [2]
RA SEQUENCE FROM N.A.
RX Xu L.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR EMBL: U25675; AAA70096.1; -.
DR HSSP: P09989; 1MR0.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0030598; F:rRNA N-glycosylase activity; IEA.
DR GO: GO:0006952; P:defense response; IEA.
DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR GO: GO:0009405; P:patogenesis; IEA.
DR InterPro: IPR001574; RIP.
DR Pfam: PF00161; RIP.
DR PRINTS: PR00396; SHIGARICIN.
DR PROSITE: PS00275; SHIGA RICIN; 1.
KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT NON_TER 270
FT TER 270
SQ SEQUENCE 270 AA; 29993 MW; 3D73FB461EA8BD4 CRC64;

Query Match 95.2%; Score 1162; DB 2; Length 270;
Best local Similarity 94.7%; Pred. No. 3e-87;
Matches 224; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy      1 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPSCQRVALIHLTNVADETI 60
Db      24 DVSFRLSGATSSSYGVFISNLRKALPYERKLYDIPILRSTLPSCQRVALIHLTNVADETI 83
Qy      61 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKVTLTPYSGNYERLQTPAGK 120
Db      84 SVAIDVTNYIMGRAGDTSYFFNEASATEAAKYVFDAMRKVTLTPYSGNYERLQTPAGK 143
Qy      121 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARAKYFIEQOIGKRVDTFL 180
Db      144 IRENIPILGIPALDSATITLTFYNNANSAALMWLIQSTSEARAKYFIEQOIGKRVDTFL 203
Qy      181 PSIAIISLNSWSALSQIOIASTNNGQFESPVLINAOQRVTITNVDAVTSNIAL 240
Db      204 PSIAIISLNSWSALSQIOIASTNNGQFETPVLLINAOQRVTITNVDAVTSNIAL 263
Qy      241 LNRNNMA 247

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Db 264 INRNMM 270

RESULT 9

Q6PRG5 PRELIMINARY; PRT; 270 AA.

AC Q6PRG5; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Trichomelin (Fragment).
 GN Name=tcml;
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid1; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxId=3677;

SEQUENCE FROM N.A.

RA Mi S., An C., Chen J., Wang Y., Yuan H., Chen Z.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AY584242; AAS92579.1; -.
 DR HSSP; P16094; IAHG.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA_RICIN; 1.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.

FT NON TER 270

SQ SEQUENCE 270 AA; 29649 MW; 5BB513B754F9B769 CRC64;

Query Match

Best Local Similarity 95.2%; Score 1162; DB 2; Length 270;
 Matches 236; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORVALIHLTNYADETI 60

Db 24 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORVALIHLTNYADETI 83

QY 61 SVAIDVTNVIYIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPSYGNVERLQTPACK 120

Db 84 SVAIDVTNVIYIMGYRAGDISYFPNEASATEAKYVFKDAMRKVTLPSYGNVERLQTPACK 143

QY 121 IRENIPILGIPALDSATITLFFYNNANSAASALMWLIOSTSEARARYFIEQIGKRDVKTFL 180

Db 144 IRENIPILGIPALDSATITLFFYNNANSAASALMWLIOSTSEARARYFIEQIGKRDVKTFL 203

QY 181 PSLAIISLSENSWSALSQIOIASTNNQGFESPVLINQONRVITINVDAGVTSNIALL 240

Db 204 PSLAIISLSENSWSALSQIOIASTNNQGFESPVLINQONRVITINVDAGVTSNIALL 263

QY 241 INRNMM 247

Db 264 INRNMM 270

RESULT 10

Q8LPV7 PRELIMINARY; PRT; 270 AA.

AC Q8LPV7; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Trichosanthin precursor (Fragment).

GN Name=TCS;
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid1; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxId=3677;

SEQUENCE FROM N.A.

RA Sun H., Wang Y., Liu T., An C., Chen Z.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL; AY082348; AAM2782.1; -.
 DR PIR; JC5032; JC5032.

DR HSSP; P09989; IMRT.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.

DR GO; GO:0006952; P:defense response; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA_RICIN; 1.

KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT CHAIN 1 23
 FT SIGNAL 1 23
 FT NON TER 270
 FT CHAIN 24 >270
 FT NON TER 270
 SQ SEQUENCE 270 AA; 29683 MW; 531713B754F9B769 CRC64;

Query Match

Best Local Similarity 94.8%; Score 1158; DB 2; Length 270;
 Matches 235; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORVALIHLTNYADETI 60

Db 24 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORVALIHLTNYADETI 83

QY 61 SVAIDVTNVIYIMGYRAGDTSYFPNEASATEAKYVFKDAMRKVTLPSYGNVERLQTPACK 120

Db 84 SVAIDVTNVIYIMGYRAGDISYFPNEASATEAKYVFKDAMRKVTLPSYGNVERLQTPACK 143

QY 121 IRENIPILGIPALDSATITLFFYNNANSAASALMWLIOSTSEARARYFIEQIGKRDVKTFL 180

Db 144 IRENIPILGIPALDSATITLFFYNNANSAASALMWLIOSTSEARARYFIEQIGKRDVKTFL 203

QY 181 PSLAIISLSENSWSALSQIOIASTNNQGFESPVLINQONRVITINVDAGVTSNIALL 240

Db 204 PSLAIISLSENSWSALSQIOIASTNNQGFESPVLINQONRVITINVDAGVTSNIALL 263

QY 241 INRNMM 247

Db 264 INRNMM 270

RESULT 11

RIP1_BRYDI STANDARD; PRT; 290 AA.

AC P33185; Q9S819; 01-OCT-1993 (Rel. 27, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ribosome-inactivating protein bryodin I precursor (EC 3.2.2.22) (rRNA
 N-glycosidase) (BDI).
 OS Bryonia dioica (Red bryony).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid1; Cucurbitales; Cucurbitaceae; Bryonia.
 OC NCBI_TaxId=3652;

SEQUENCE FROM N.A., MUTAGENESIS OF GLU-212, AND X-RAY CRYSTALLOGRAPHY
 RP (2.1 ANGSTROMS).

RC TISSUE=leaf;
 RX MEDLINE=97228081; PubMed=9115985; DOI=10.1021/b1962474+;
 RA Siegal C.B.; Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.,
 RT "Molecular, biological, and preliminary structural analysis of
 RT recombinant bryodin 1, a ribosome-inactivating protein from the plant
 RT Bryonia dioica.";
 RL Biochemistry 36:3095-3103(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Siegal C.B.;
 RT "Cloning and expression of a gene encoding bryodin 1 from Bryonia
 RT dioica.";
 RL Patent number US5541110, 30-JUL-1996.
 RN [3]
 RP SEQUENCE OF 24-66.
 RX MEDLINE=89326691; PubMed=2753596;
 RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
 RA Lippi D.;
 RT "N-terminal sequence of some ribosome-inactivating proteins.";
 RL Int. J. Pept. Protein Res. 33:263-267(1989).
 RN [4]
 RP SEQUENCE OF 24-43.
 RX MEDLINE=95151812; PubMed=7848072;
 RA Margardt H.; Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
 RT "Characterization of ribosome-inactivating proteins isolated from
 RT Bryonia dioica and their utility as carcinoma-reactive
 RT immunocjugates.";
 RL Bioconj. Chem. 5:423-429(1994).
 CC -1- FUNCTION: Ribosome-inactivating protein of type 1, inhibits
 CC protein synthesis in animal cells.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- PTM: Appears to undergo proteolytic cleavage in the C-terminal to
 CC produce a shorter protein.
 CC -1- BIOTECHNOLOGY: Especially useful as immunotoxin for
 CC pharmacological applications as it has low toxicity in rats and
 CC mice but is potent once inside target cells.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.
 CC -----
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL; I24020; -; NOT_ANNOTATED_CDS.
 CC PIR; S16491; S16491.
 DR PDB; 1BRV; X-ray; Y/Z=23-270.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KM 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
 KM Multigene family; Plant defense; Protein synthesis inhibitor; Signal;
 KM Toxin.
 FT STGNAL 1 23
 FT CHAIN 24 270
 FT PROPEP 271 290
 FT ACT SITE 183 183
 FT ACT SITE 212 212
 FT CARBOHYD 214 214
 FT CARBOHYD 250 250
 FT MUTAGEN 212 212
 FT CONFICT 61 65
 FT STRAND 25 28
 FT TURN 30 31

FT HELIX 34 46
 FT TURN 47 47
 FT STRAND 50 54
 FT TURN 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 69
 FT STRAND 70 76
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 89 92
 FT STRAND 93 99
 FT TURN 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT TURN 115 117
 FT TURN 120 121
 FT STRAND 124 127
 FT STRAND 134 141
 FT HELIX 142 142
 FT TURN 145 147
 FT STRAND 150 150
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 FT TURN 226 230
 FT STRAND 231 239
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 FT HELIX 254 257
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 FT STRAND 260 260
 FT STRAND 263 263
 FT HELIX 266 268
 SQ SEQUENCE 290 AA; 31788 MW; E966CD9C031A42DB CRC64;
 Query Match 87.7%; Score 1071; DB 1; Length 290;
 Best Local Similarity 86.2%; Pred. No. 9,7e-80;
 Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DVSPRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPQSORVALIHLTNVADDTI 60
 DB 24 DVSPRLSGATTSYGVFINKRLALPYERKVINIPILRSSISGGRYTLHLTNVADDTI 83
 QY 61 SVAIDVTNYVIMGYRAGDTSYFPENASATEAAKYVFKDARKVTLPYSGNYERLQTPACK 120
 DB 84 SVAVDVTNYVIMGYLAGDVSYPFENASATEAAKFVKDARKVTLPYSGNYERLQTPACK 143
 QY 121 IRENIFLPGPALDSATITLFPYANASASALMWLIDSTSEARKYFIEQOIGKRVKTF 180
 DB 144 IRENIFLPGPALDSATITLFPYANASASALMWLIDSTSEARKYFIEQOIGKRVKTF 203
 QY 181 PSIAITSLSENSWALSQKQIQTSTNGOFESPVLINANORVTTINVDAGVTSNIAL 240
 DB 204 PSIAITSLSENSWALSQKQIQTSTNGOFESPVLINANORVTTINVDAGVTSNIAL 263
 QY 241 LNRNNNA 247
 DB 264 LNRNNNA 270
 RESULT 12
 RIPL_MOMCH STANDARD; PRT; 286 AA.
 ID RIPL_MOMCH
 AC P16094; P24697;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 25-OCT-2004 (rel. 45, last annotation update)

DE Ribosome-inactivating protein momordin I precursor (EC 3.2.2.22) (rRNA

DB N-glycosidase) (Alpha-momorcharin) (Alpha-MMC).

OS Momordica charantia (Bitter melon) (Balsam pear).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.

NCBI_Taxid=3673;

CC [1] _____

CC SEQUENCE FROM N.A.

CC TISSUE=Seed;

CC MEDLINE=91159486; PubMed=2001404; DOI=10.1016/0167-4781(91)90070-3;

CC Ho W.K.K., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;

CC "Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating

CC protein.";

CC Biochim. Biophys. Acta 1088:311-314 (1991).

CC [2] _____

CC SEQUENCE OF 24-38.

CC TISSUE=Seed;

CC MEDLINE=89326691; PubMed=2753596;

CC Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,

CC Lapi D.;

CC "N-terminal sequence of some ribosome-inactivating proteins.";

CC Int. J. Pept. Protein Res. 33:263-267 (1989).

CC [3] _____

CC SEQUENCE OF 24-70.

CC TISSUE=Seed;

CC MEDLINE=89005108; PubMed=3262509;

CC Casellas P., Dussosoy D., Palasca A.I., Barbieri L., Guillemot J.C.,

CC Ferrara P., Bolognesi A., Cenini P., Stirpe F.;

CC "Trichostatin, a ribosome-inactivating protein from the seeds of

CC Trichosanthes kirilowii Maximowicz. Purification, partial

CC characterization and use for preparation of immunotoxins.";

CC Eur. J. Biochem. 176:581-588 (1988).

CC [4] _____

CC X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

CC MEDLINE=94356447; PubMed=8075985;

CC Ren J., Wang Y., Dong Y., Stuart D.I.;

CC "The N-glycosidase mechanism of ribosome-inactivating proteins implied

CC by crystal structures of alpha-momorcharin.";

CC Structure 2:7-16 (1994).

CC [5] _____

CC X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).

CC MEDLINE=94192822; PubMed=8143869; DOI=10.1016/0014-5793(94)80491-5;

CC Husain J., Tickle I.J., Wood S.P.;

CC "Crystal structure of momordin, a type I ribosome inactivating protein

CC from the seeds of Momordica charantia.";

CC FEBS Lett. 342:154-158 (1994).

CC [6] _____

CC X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

CC MEDLINE=95344383; PubMed=7619070;

CC Huang Q., Liu S., Tang Y., Jin S., Wang Y.;

CC "Studies on crystal structures, active-centre geometry and

CC dehydrating mechanism of two ribosome-inactivating proteins.";

CC Biochem. J. 309:285-298 (1995).

CC [7] _____

CC CARLYLYRIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

CC specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.

CC Type 1 RIP subfamily.

CC -----

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CC -----

CC EMBL; X57682; CAA0869.1; -

CC PIR; S14273; RLPUG

CC PDB; 1AH4; X-ray; @=24-269.

CC PDB; 1AHB; X-ray; @=24-269.

CC PDB; 1AHC; X-ray; @=24-269.

DR PDB; 1F8Q; X-ray; A=24-286.

DR PDB; 1MOM; X-ray; @=24-269.

DR PDB; 1MRG; X-ray; @=24-286.

DR PDB; 1MRH; X-ray; @=24-286.

DR PDB; 1MRI; X-ray; @=24-286.

DR GlycoSiteDB; P16094; -

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA_RICIN; 1.

KM 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;

KM Plant defense; Protein synthesis inhibitor; Signal; Toxin.

FT SIGNAL 1 23

FT CHAIN 24 269

FT PROPEP 270 286

FT ACT SITE 183 183

FT CAROXYD 250 250

FT STRAND 25 28

FT HELIX 34 47

FT STRAND 50 54

FT TURN 55 56

FT STRAND 57 60

FT HELIX 66 69

FT STRAND 70 76

FT TURN 78 79

FT STRAND 82 88

FT TURN 89 92

FT STRAND 93 99

FT TURN 100 101

FT STRAND 102 105

FT HELIX 109 114

FT TURN 115 117

FT TURN 120 121

FT STRAND 124 127

FT HELIX 134 141

FT HELIX 145 147

FT STRAND 150 150

FT HELIX 152 162

FT TURN 163 163

FT HELIX 167 186

FT STRAND 187 187

FT HELIX 188 195

FT TURN 196 197

FT STRAND 202 202

FT HELIX 206 225

FT TURN 226 230

FT STRAND 231 238

FT TURN 240 241

FT STRAND 246 250

FT TURN 251 252

FT HELIX 254 258

FT TURN 259 259

FT STRAND 260 260

FT STRAND 263 263

FT HELIX 266 268

SQ SEQUENCE 286 AA; 31532 MW; E1B013ABBC216CF CRC64;

Query Match 65.7%; Score 802; DB 1; Length 286;

Best Local Similarity 65.2%; Pred. No. 1.2e-57;

Matches 161; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

Qy 1 DVSPRLSGATSSSYVPTISNRKALPNERKLYDPIPLSSLPDGSORVALIHVTYADPTI 60

Db 24 DVSPRLSGADPRSYGMFKDRLNALPPEKRYNIPLLPSVSGARVYLMHLFNTDGKTI 83

Qy 61 SVADIVTVVYIMGYRAGDTSYFPEASATEAKVYFKDAMRKVTLPSGNYERLQTAAGK 120

Db 84 TVAVDVTVVYIMGYRAGDTSYFPEASATEAKVYFKDAMRKVTLPSGNYERLQTAAGK 143

Qy 121 IRENIPDLGPAIDSAITTLFYNNANSAASALMVLIOSTSEARKYFIQOIGKRVDTFL 180

Db 144 PREKIPDGLPDLDSAISTLTHYDSTAAAGALLVLIQTVAEAAARFXYIEQOIERAYRDEV 203


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QY 181 PSLAIIISLSEWSKSLAKXIOIJAISTNGGFESEVVLINAKONRVLTIVNDAVYVSNIALI 240
Db 204 PSLAIIISLSEWSKSLAKXIOIJAQGNNGIFRPIVLVDNKNRVOITVNTSVTSNIQLL 263
QY 241 LNRNNMA 247
Db 264 LNRNRIA 270

RESULT 13
RIPA_LUFCY STANDARD; PRT; 277 AA.
AC 000465;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Ribosome-inactivating protein luffin-alpha precursor (EC 3.2.2.22)
DE (rRNA N-glycosidase).
OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eusterois 1; Cucurbitales; Cucurbitaceae; Luffa.
OX NCBI_TaxID=3670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed.
RX MEDLINE=92288316; PubMed=1600156;
RA Kataoka J., Habuka N., Miyano M., Masuta C., Koizumi A.;
RT "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
RT inactivating protein from Luffa cylindrica."
RL Plant Mol. Biol. 18:1199-1202(1992).
CC -1- CARBAMYLIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC Type 1 RIP subfamily.
CC -----
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CC -----
DR EMBL; X62371, CAA44229.1; -.
DR PIR; S22494; S22494.
DR HSSP; P16094; IAHG.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Antiviral; Hydrolase; Plant defense; Protein synthesis inhibitor;
KW Signal; Toxin.
FT SIGNAL 1 19
FT CHAIN 20 277
FT FT 19 Ribosome-inactivating protein luffin-
FT alpha.
FT ACT SITE 179 179 By similarity.
FT SO SEQUENCE 277 AA; 30212 MW; EAL7FC27998C25AC CRC64;

Query Match 61.8%; Score 754; DB 1; Length 277;
Best Local Similarity 62.1%; Pred. No. 9.7e-54;
Matches 154; Conservative 42; Mismatches 50; Indels 2; Gaps 2;

QY 1 DVSFPLSGATSSSYGVFISNLRKALPNERKLYDIFLASSLPDGSGRVYLLHLYTADBTI 60
Db 21 DVRFSLSSSSSTSYKFTGDRKALPNSGTYNYNTITLLSSASGASRYTILMTLSNDGVAI 80
QY 61 SVAIDVTWVYIMYGACDTSYFFENSASTEAKYVFKDAMRKVTLTPYSGNTERLQTAGK 120
Db 81 TVAVDVTVYIMYGIVNSTSYFPNESAQVYFKKS -RTVLPYSGNTERLQTAGK 139
QY 121 IRENIPGLPALDAITTLTFYNNANSAASALMWLIQSTSEARVYKEIEQIIGKRVDTKL 180

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Db	140	IREKTIPLGFPALDSDAITLTFHYDSTAAALAAFLVITQTAAASRFKXIEGQILTERISKQV	199
Qy	181	PSLAIIISLNSWSALSOKIOIAISTNNGCFESPVPVLINANORVTTITNDAGVTSINALL	240
Db	200	PSLATTISLNSWMSALSOKIOIAQNTNNGTFKTPVVTITDDKQGVETITNVTSSKVFTKNIQL	259
Qy	241	LN-RNMA 247	
Db	260	LNKONVA 267	
RESULT 14			
ID	000980	PRELIMINARY; PRT; 278 AA.	
AC	000980;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	B-luffin.		
OS	Luffa cylindrica (Smooth loofeh) (Sponge gourd).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	Eurosoids I; Cucurbitales; Cucurbitaceae; Luffa.		
OX	NCHI_TaxID=3670;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=92286316; PubMed=1600156;		
RA	Kataoka Y., Habuka N., Miyano M., Masuta C., Koizai A.;		
RT	"Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-		
RL	inactivating protein from Luffa cylindrica."		
RL	Plant Mol. Biol. 18:1199-1202(1992).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=92353400; PubMed=1643290;		
RA	Kataoka Y., Habuka N., Miyano M., Masuta C., Koizai A.;		
RT	"Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-		
RL	inactivating protein from Luffa cylindrica."		
RL	Plant Mol. Biol. 19:887-889(1992).		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one		
CC	specific adenosine on the 28S rRNA.		
CC	-1- SIMILARITY: Belongs to the ribosome-inactivating protein family.		
DR	EMBL; X62372; CA444230.1; -		
DR	PIR; S23519; S23519.		
DR	HSSP; P22851; INFO.		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.		
DR	GO; GO:0006952; P:defense response; IEA.		
DR	GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR001574; RIP.		
DR	Pfam; PF00161; RIP; 1.		
DR	PRINTS; PR00396; SHIGARICIN.		
DR	PROSITE; PS00275; SHIGA_RICIN; 1.		
KW	Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.		
SEQ	SEQUENCE 278 AA; 30586 MW; 40C26576B53B850 CRC64;		
Query Match 59.7%; Score 728.5; DB 2; Length 278;			
Best local Similarity 59.9%; Pred. No.1.2e-51;			
Matches 148; Conservative 44; Mismatches 54; Indels 1; Gaps 1			
Qy	1	DVSFPLSGATSSGVFISNLRKALPNERKLYDIPLASSLPGSORVALIHHTNVADETI	60
Db	23	NVSSSLSGADSKSISKFTTLARKALPSKEKSNIPDLPPSAGARITLMOLSNDAKAI	82
Qy	61	SVADIVTVNYTMGYRAGDTSYFPEASATEAKYVFKDAMRKVTLPSYGNTERTLTAAAG	120
Db	83	TMAIDIVTVNYTMGYLVNSTSYFPEASDAKLASQYVFKGS-TIVLPYSGNTERLTQNAAGK	141
Qy	121	IRENIPGLPLADSAITLTFYNNNSASALMLTIQSTSEARARYFTIEQIGKRDVTFLL	180
Db	142	VREKIPGFEFRFSDAITSLSLHYDSTAAAGAFVLIIQTAAASRFKXIEGQILTERIPKNEV	201

QY 181 PSIAISLSENSWALSKOIOIASTNNGQFSPVYLINAQNRVTINNDAGVTSINAIL 240
 DB 202 PSPAALSLSENSWALSKOIOIAQTNNGAFRTPVVILIDNKQFVEIKDVNSKVITNNIKLL 261
 QY 241 LNRNNMA 247
 DB 262 LNKQNTA 268

Search completed: April 12, 2005, 15:13:59
 Job time : 107.91 secs

RESULT 15

0684J5 PRELIMINARY; PRT; 264 AA.
 AC 0684J5;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Type I ribosome inactivating protein precursor (Fragment).
 GN Name=rip;
 OS Momordica charantia (Bitter melon) (Balsam pear).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
 OX NCBI_TaxID=3673;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,
 RA Tran Thi Phuong L., Nong Van H.;
 RT "Expression of a gene encoding ribosome inactivating protein from
 RT bitter melon (Momordica charantia).";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Nong V.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -! SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC EMBL; AJ748278; CAH19208.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolyase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT NON_TER 1 1
 FT SIGNAL <1 1 Potential.
 FT CHAIN 2 264 type I ribosome inactivating protein.
 SQ SEQUENCE 264 AA; 29775 MW; AD9E1175B70521AD CRC64;

Query Match 58.2%; Score 711; DB 2; Length 264;
 Best Local Similarity 61.6%; Pred. No. 3.1e-50;
 Matches 149; Conservative 31; Mismatches 60; Indels 2; Gaps 2;

QY 1 DVSFRLSGATSSSYGFIINLRKALPNERKLYDIPILRSSLPQSGRYALIHLYNADETI 60
 DB 2 DVNPFDSLSTAYAKYTFIEDFRATLPFSKVVYDIPLLYSTISDSRRFILNLTSYAVETI 61
 QY 61 SVAIDVTNYVINGYRAGDTSYFENEASATEAAKYVFKDMARKVTLPYSGNVERLQTAAGK 120
 DB 62 SVAIDVTNYVAVYRTRDVSYPFKE-SPEBAVNIIRK-GTRKTLTPYTGNYENTLQTAHK 119
 QY 121 IRENIPUGLPALDSAITTLFFYNANSASALNVLIOSTSEAAKYKEIEQOIGKRVDTFL 180
 DB 120 IRENIDLG.PALSSAITTLFFYNAQSPALVLIOGTAARFXYIERHVAKYVATNPK 179
 QY 181 PSIAISLSENSWALSKOIOIASTNNGQFSPVYLINAQNRVTINNDAGVTSINAIL 240
 DB 180 PNLAIISLENQWALSKOILFLAQNQGGKFRNPVDLIKPTGERFQVTNVDSDVVKENIKLL 239
 QY 241 LN 242
 DB 240 LN 241

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OM protein - protein search, using sw model

Run on: April 12, 2005, 15:14:19 ; Search time 95.4347 Seconds
(without alignments)
1005.370 Million cell updates/sec

Title: US-09-905-247A-1
Perfect score: 1431
Sequence: 1 MIRFLVSLILTLFLTPA.....AAMDVVPMVQSGCGSYAL 289

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      1418010 seqs, 331997259 residues
Total number of hits satisfying chosen parameters: 1418010

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Maximum DB seq length: 20000000000

Post-processing:	Minimum Match	0%
	Maximum Match	100%

Database : Published Applications AA:

Published applications AA: *

- 1: /cgn2_6/prodataa1/pubppaa/US07_PUBCOMB_dep: *
- 2: /cgn2_6/prodataa1/pubppaa/PCT_NEW_PUB_dep: *
- 3: /cgn2_6/prodataa1/pubppaa/US06_NEW_PUB_dep: *
- 4: /cgn2_6/prodataa1/pubppaa/US06_PUBCOMB_dep: *
- 5: /cgn2_6/prodataa1/pubppaa/US07_NEW_PUB_dep: *
- 6: /cgn2_6/prodataa1/pubppaa/PCTUS_PUBCOMB_dep: *
- 7: /cgn2_6/prodataa1/pubppaa/US08_NEW_PUB_dep: *
- 8: /cgn2_6/prodataa1/pubppaa/US08_PUBCOMB_dep: *
- 9: /cgn2_6/prodataa1/pubppaa/US09_PUBCOMB_dep: *
- 10: /cgn2_6/prodataa1/pubppaa/US09_PUBCOMB_dep: *
- 11: /cgn2_6/prodataa1/pubppaa/US09C_PUBCOMB_dep: *
- 12: /cgn2_6/prodataa1/pubppaa/US09_NEW_PUB_dep: *
- 13: /cgn2_6/prodataa1/pubppaa/US10A_PUBCOMB_dep: *
- 14: /cgn2_6/prodataa1/pubppaa/US10B_PUBCOMB_dep: *
- 15: /cgn2_6/prodataa1/pubppaa/US10C_PUBCOMB_dep: *
- 16: /cgn2_6/prodataa1/pubppaa/US10_PUBCOMB_dep: *
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- 18: /cgn2_6/prodataa1/pubppaa/US11_NEW_PUB_dep: *
- 19: /cgn2_6/prodataa1/pubppaa/US60_NEW_PUB_dep: *
- 20: /cgn2_6/prodataa1/pubppaa/US60_PUBCOMB_dep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1424	99.5	289	11	US-09-980-247-1	Sequence 1, Appl1
2	1420	99.2	289	15	US-10-280-679B-4	Sequence 4, Appl1
3	1420	99.2	289	15	US-10-280-775B-4	Sequence 4, Appl1
4	1221	85.3	247	9	US-09-792-793A-39	Sequence 39, Appl1
5	1221	85.3	247	15	US-10-375-209A-39	Sequence 39, Appl1
6	1209	84.5	247	14	US-10-127-890-6	Sequence 6, Appl1
7	1209	84.5	247	17	US-10-717-243-6	Sequence 6, Appl1
8	1071	74.8	247	9	US-09-792-793A-34	Sequence 34, Appl1
9	1071	74.8	247	15	US-10-375-209A-34	Sequence 34, Appl1
10	813.5	56.8	263	14	US-10-127-890-7	Sequence 7, Appl1
11	813.5	56.8	263	17	US-10-717-243-7	Sequence 7, Appl1
12	724.5	50.6	248	14	US-10-127-890-5	Sequence 5, Appl1
13	724.5	50.6	248	17	US-10-717-243-5	Sequence 5, Appl1

14	709	49.5	263	14	US-10-127-890-4	Sequence 4, Appl 1
15	709	49.5	263	17	US-10-717-243-4	Sequence 4, Appl 1
16	421	29.4	267	14	US-10-282-933-1	Sequence 1, Appl 1
17	421	29.4	267	14	US-10-127-890-1	Sequence 1, Appl 1
18	421	29.4	267	15	US-10-440-796-1	Sequence 1, Appl 1
19	421	29.4	267	17	US-10-717-243-1	Sequence 1, Appl 1
20	421	29.4	576	14	US-10-083-336-1	Sequence 1, Appl 1
21	342	23.9	198	14	US-10-083-336-3	Sequence 3, Appl 1
22	342	23.9	198	14	US-10-083-336-5	Sequence 7, Appl 1
23	342	23.9	199	14	US-10-083-336-6	Sequence 5, Appl 1
24	342	23.9	200	14	US-10-083-336-9	Sequence 10, Appl 1
25	337.5	23.6	185	14	US-10-083-336-9	Sequence 9, Appl 1
26	336	23.5	188	14	US-10-083-336-4	Sequence 4, Appl 1
27	336	23.5	188	14	US-10-083-336-6	Sequence 8, Appl 1
28	336	23.5	189	14	US-10-083-336-8	Sequence 6, Appl 1
29	336	23.5	190	14	US-10-083-336-11	Sequence 11, Appl 1
30	330	23.1	251	14	US-10-282-933-3	Sequence 3, Appl 1
31	330	23.1	251	15	US-10-440-796-3	Sequence 3, Appl 1
32	330	23.1	293	9	US-09-765-527-259	Sequence 259, App
33	330	23.1	309	9	US-09-765-527-253	Sequence 253, App
34	330	22.8	332	9	US-09-765-527-251	Sequence 251, App
35	326	22.8	252	9	US-09-347-064-2	Sequence 2, Appl 1
36	326	22.8	252	9	US-09-347-064-8	Sequence 8, Appl 1
37	323	22.6	251	14	US-10-127-890-99	Sequence 99, Appl 1
38	323	22.6	251	14	US-10-127-890-101	Sequence 101, Appl 1
39	323	22.6	251	14	US-10-127-890-107	Sequence 107, Appl 1
40	323	22.6	251	17	US-10-717-243-99	Sequence 99, Appl 1
41	323	22.6	251	17	US-10-717-243-101	Sequence 101, Appl 1
42	323	22.6	251	17	US-10-717-243-107	Sequence 107, App
43	322	22.5	251	14	US-10-127-890-110	Sequence 110, App
44	322	22.5	251	14	US-10-127-890-111	Sequence 111, App
45	322	22.5	251	17	US-10-717-243-110	Sequence 110, App

ALIGNMENTS

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RESULT
US-09-905-247-1
? Sequence 1, Application US/09905247
? Publication No. US20040197853A1
? GENERAL INFORMATION:
? APPLICANT: KE, YI-BAO
? APPLICANT: NIE, HUI-LING
? TITLE OR INVENTION: Mutant Trichosanthes
? FILE REFERENCE: 04399/000J615-USO
? CURRENT APPLICATION NUMBER: US/09/905.2
? CURRENT FILING DATE: 2001-07-13
? PRIOR APPLICATION NUMBER: CN 00119553.C
? PRIOR FILING DATE: 2000-08-02
? PRIOR APPLICATION NUMBER: CN 01103102.6
? PRIOR FILING DATE: 2001-01-18
? NUMBER OF SEQ ID NOS: 7
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 1
? LENGTH: 289
? TYPE: FRT
? ORGANISM: Trichosanthes Kirtlowii M.
US-09-905-247-1

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Best Local Similarity	99.7%	Pred. No. 1,2e-128		
Matches 288	Conservative	0	Mismatches 1	Indels 0
QY	1	MIRELTLTLTLTFLTPPAVEGDVSFPLSGATSSSYVFISNDRLKLPNERKLYDIPLL	60	
Db	1	MIRFVLSLTLTLTFLTPPAVEGDVSFPLSGATSSSYVFISNRLKLPNERKLYDIPLL	60	
QY	61	RSSLPSQSYVALIHLTNVADETSVAIDVTNVYIMGYAGDTSYFFPEASATAEAKVFK	120	
Db	61	RSSLPSQSYVALIHLTNVADETSVAIDVTNVYIMGRPADGTSYFFPGASATAEAKVFK	120	
QY	121	DAMKVTLPESGNYERLQTAAGIKRENIPLGIPLDLSATITLLFYNNANSAASALMVIQS	180	

Db 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSAITTLFFYNNANSAASALMWLIOS 180
QY 181 TSEAAKYKFEIOQIGKRVKTFPLPSLAITISLENSWSALSKOIOIASTNNQGFESPVVLIN 240
Db 181 TSEAAKYKFEIOQIGKRVKTFPLPSLAITISLENSWSALSKOIOIASTNNQGFESPVVLIN 240
QY 241 AONORVTITNVDAVGVTSNIALLLNRRNNMAAMDDVPMTOFSGCGSYAL 289
Db 241 AONORVTITNVDAVGVTSNIALLLNRRNNMAAMDDVPMTOFSGCGSYAL 289
RESULT 2
US-10-280-679B-4
; Sequence 4, Application US/10280679B
; Publication No. US20030150019A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Monoparticle RNA Virus Transformation Vectors
; FILE REFERENCE: LSBC-0109-US03
; CURRENT APPLICATION NUMBER: US/10/280,679B
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/557,941
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 08/484,341
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600,244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641,617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737,899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739,143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310,881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160,766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160,771
; PRIOR FILING DATE: 1988-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 289
; TYPE: PR1
; ORGANISM: Chinese cucumber protein alpha-trichosanthin
US-10-280-679B-4
Query Match 99.2%; Score 1420; DB 14; Length 289;
Best Local Similarity 99.0%; Pred. No. 2.8e-128;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIRFVLISLILITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60
Db 1 MIRFVLISLILITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60
QY 61 RSLPSGQRYALIHLTNVADETSVAIDVTNVYIMGYRAGDTSYFENEASATEAKYVFK 120
Db 61 RSLPSGQRYALIHLTNVADETSVAIDVTNVYIMGYRAGDTSYFENEASATEAKYVFK 120
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Db 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSAITTLFFYNNANSAASALMWLIOS 180
QY 181 TSEAAKYKFEIOQIGKRVKTFPLPSLAITISLENSWSALSKOIOIASTNNQGFESPVVLIN 240
Db 181 TSEAAKYKFEIOQIGKRVKTFPLPSLAITISLENSWSALSKOIOIASTNNQGFESPVVLIN 240
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RESULT 3
US-10-280-725B-4
; Sequence 4, Application US/10280725B
; Publication No. US20040049025A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Recombinant Viral Nucleic Acids
; FILE REFERENCE: LSBC-0109-US02
; CURRENT APPLICATION NUMBER: US/10/280,725B
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/557,941
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 08/484,341
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600,244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641,617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737,899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739,143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310,881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160,766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160,771
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 289
; TYPE: PR1
; ORGANISM: Chinese cucumber
US-10-280-725B-4
Query Match 99.2%; Score 1420; DB 15; Length 289;
Best Local Similarity 99.0%; Pred. No. 2.8e-128;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIRFVLISLILITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60
Db 1 MIRFVLISLILITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60
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Db 61 RSLPSGQRYALIHLTNVADETSVAIDVTNVYIMGYRAGDTSYFENEASATEAKYVFK 120
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RESULT 4
US-09-792-793A-39
; Sequence 39, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.

APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosantheus kirilowii
US-09-792-793A-39

Query Match 85.3%; Score 1221; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.4e-109;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SVAIDVTNVIIMGYRAGDTSYFFNEASATEAAKYVFDAMRKTYLTPYSGYVERLQTAAGK 120
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DB 121 IRENIPGLPALDSAITTLFFYNANSASALMWLIGSTSEAAKYKFEQOIGKRVDTFL 180
QY 204 PSIAIISLENSWSALSQIOIASITNGOFESPVLINAOQRTITNVADGVTSNIAL 263
DB 181 PSIAIISLENSWSALSQIOIASITNGOFESPVLINAOQRTITNVADGVTSNIAL 240
QY 264 LNRNMA 270
DB 241 LNRNMA 247

RESULT 5
US-10-375-209A-39
Sequence 39, Application US/10375209A
Publication No. US20030215421A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601E
CURRENT APPLICATION NUMBER: US/10/375,209A
CURRENT FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosantheus kirilowii
US-10-375-209A-39

Query Match 85.3%; Score 1221; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.4e-109;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSLSLPGSORYALHLTNVADETI 83
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSLSLPGSORYALHLTNVADETI 60
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DB 61 SVAIDVTNVIIMGYRAGDTSYFFNEASATEAAKYVFDAMRKTYLTPYSGYVERLQTAAGK 120
QY 144 IRENIPGLPALDSAITTLFFYNANSASALMWLIGSTSEAAKYKFEQOIGKRVDTFL 203

DB 121 IRENIPGLPALDSAITTLFFYNANSASALMWLIGSTSEAAKYKFEQOIGKRVDTFL 180
QY 204 PSIAIISLENSWSALSQIOIASITNGOFESPVLINAOQRTITNVADGVTSNIAL 263
DB 181 PSIAIISLENSWSALSQIOIASITNGOFESPVLINAOQRTITNVADGVTSNIAL 240
QY 264 LNRNMA 270
DB 241 LNRNMA 247

RESULT 6
US-10-127-890-6

Sequence 6, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70,P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-127-890-6

Query Match 84.5%; Score 1209; DB 14; Length 247;
Best Local Similarity 99.2%; Pred. No. 4.9e-108;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSLSLPGSORYALHLTNVADETI 83

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QY      84 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKFDMARKVTLPSYSGNYERLQTAAGK 143
Db      61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKFDMARKVTLPSYSGNYERLQTAAGK 120
QY      144 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYKFEIQIGKRVDTKFTL 203
Db      121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYKFEIQIGKRVDTKFTL 180
QY      204 PSIAIISLNSWSALSQKQIQIASTNNGQPESPVLINQONQRTITNVDAVVTSNIALL 263
Db      181 PSIAIISLNSWSALSQKQIQIASTNNGQPESPVLINQONQRTITNVDAVVTSNIALL 240
QY      264 LNRNNMA 270
Db      241 LNRNNMA 247
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RESULT 7

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US-10-717-243-6
; Sequence 6, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
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APPLICANT: Better, Marc D.
Carroll, Stephen F.
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Studnika, Gary M.
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TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
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```
Proteins
```

```
NUMBER OF SEQUENCES: 169
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```
CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
```

```
STREET: 500 West Madison Street, 34th floor
```

```
CITY: Chicago
```

```
STATE: Illinois
```

```
COUNTRY: USA
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ZIP: 60661
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COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: IBM PC compatible
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SOFTWARE: Patent in Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/10/717,243
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FILING DATE: 18-Nov-2003
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CLASSIFICATION: 530
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/08/839,765
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FILING DATE: 15-APR-1997
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APPLICATION NUMBER: US 08/425,336
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FILING DATE: 18-APR-1995
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APPLICATION NUMBER: US 08/064,691
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FILING DATE: 12-MAY-1993
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APPLICATION NUMBER: US 07/988,430
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FILING DATE: 09-DEC-1992
```

```
APPLICATION NUMBER: US 07/901,707
```

```
FILING DATE: 19-JUN-1992
```

```
APPLICATION NUMBER: US 07/787,567
```

```
FILING DATE: 04-NOV-1991
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ATTORNEY/AGENT INFORMATION:
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```
NAME: McNicholas, Janet M.
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REGISTRATION NUMBER: 32,918
```

```
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
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TELECOMMUNICATION INFORMATION:
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TELEPHONE: 312/707-8889
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TELEFAX: 312/707-9155
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TELEX: 650 388-1248
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INFORMATION FOR SEQ ID NO: 6:
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SEQUENCE CHARACTERISTICS:
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LENGTH: 247 amino acids
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TYPE: amino acid
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TOPOLOGY: linear
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MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-717-243-6
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Query Match      84.5%; Score 1209; DB 17; Length 247;
Best Local Similarity 99.2%; Pred. No. 4.9e-108;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db      1 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSRVALIHLTNVADETI 60
QY      84 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKFDMARKVTLPSYSGNYERLQTAAGK 143
Db      61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKFDMARKVTLPSYSGNYERLQTAAGK 120
QY      144 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYKFEIQIGKRVDTKFTL 203
Db      121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYKFEIQIGKRVDTKFTL 180
QY      204 PSIAIISLNSWSALSQKQIQIASTNNGQPESPVLINQONQRTITNVDAVVTSNIALL 263
Db      181 PSIAIISLNSWSALSQKQIQIASTNNGQPESPVLINQONQRTITNVDAVVTSNIALL 240
QY      264 LNRNNMA 270
Db      241 LNRNNMA 247
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RESULT 8

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US-09-792-793A-34
; Sequence 34, Application US/09792793A
; Patent No. US20020168370A1
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GENERAL INFORMATION:
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APPLICANT: McDonald, John R.
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APPLICANT: Coggin, Philip
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
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FILE REFERENCE: 25020-601D
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```
CURRENT APPLICATION NUMBER: US/09/792,793A
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NUMBER OF SEQ ID NOS: 93
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SOFTWARE: Patent in Ver. 2.0
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SEQ ID NO 34
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LENGTH: 247
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TYPE: PRT
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ORGANISM: Bryonia dioica
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US-09-792-793A-34
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Query Match      74.8%; Score 1071; DB 9; Length 247;
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Best Local Similarity 86.2%; Pred. No. 9.9e-95;
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Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
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QY      24 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSRVALIHLTNVADETI 83
Db      1 DVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPQSRVALIHLTNVADETI 60
QY      84 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKFDMARKVTLPSYSGNYERLQTAAGK 143
Db      61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKFDMARKVTLPSYSGNYERLQTAAGK 120
QY      144 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYKFEIQIGKRVDTKFTL 203
Db      121 IRENIPGLPALDSAITTLFFYNNANSASALMWLIQSTSEARRYKFEIQIGKRVDTKFTL 180
QY      204 PSIAIISLNSWSALSQKQIQIASTNNGQPESPVLINQONQRTITNVDAVVTSNIALL 263
Db      181 PSIAIISLNSWSALSQKQIQIASTNNGQPESPVLINQONQRTITNVDAVVTSNIALL 240
QY      264 LNRNNMA 270
Db      241 LNRNNMA 247
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RESULT 9
US-10-375-209A-34
Sequence 34, Application US/10375209A
Publication No. US20030215421A1
GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggin, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
FILE REFERENCE: 25020-601E
CURRENT FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 247
TYPE: PRT
ORGANISM: Bryonia dioica
US-10-375-209A-34

Query Match 74.8%; Score 1071; DB 15; Length 247;
Best Local Similarity 86.2%; Pred. No. 9.9e-95;
Matches 213; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 24 DVSEFLSGATSSSYGVFISNLRKALPNERKLYDIPILRSLSPPSGRYALHILTNVADDT 83
1 DVSEFLSGATTSYGVFISNLRKALPNERKLYDIPILRSLSPPSGRYALHILTNVADDT 60
DB 84 SVAIDVTNYIMGYRAGDTSYFFNEASATEAAKYVFKDMARKYTLPSYGNVERLQTPACK 143
61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAAKYVFKDMARKYTLPSYGNVERLQTPACK 120
QY 144 IRENIPILG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKTEBOQIGKRVKXFTL 203
121 IRENIPILG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKTEBOQIGKRVKXFTL 180
DB 204 PSIAITISLNSWSALSKQIQIASTNNGQFESPVLINAQNRVTITNVDAVGTSTNIAL 263
181 PSIAITISLNSWSALSKQIQIASTNNGQFESPVLINAQNRVTITNVDAVGTSTNIAL 240
QY 264 LNRNNMA 270
241 LNRNNMA 247
DB

RESULT 10
US-10-127-890-7
Sequence 7, Application US/10127890
Publication No. US2003016196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-127-890-7

Query Match 56.8%; Score 813.5; DB 14; Length 263;
Best Local Similarity 63.8%; Pred. No. 7.2e-70;
Matches 166; Conservative 38; Mismatches 55; Indels 1; Gaps 1;

QY 24 DVSEFLSGATSSSYGVFISNLRKALPNERKLYDIPILRSLSPPSGRYALHILTNVADDT 83
1 DVSEFLSGADPSYGVFISNLRKALPNERKLYDIPILRSLSPPSGRYALHILTNVADDT 60
DB 84 SVAIDVTNYIMGYRAGDTSYFFNEASATEAAKYVFKDMARKYTLPSYGNVERLQTPACK 143
61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAAKYVFKDMARKYTLPSYGNVERLQTPACK 120
QY 144 IRENIPILG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKTEBOQIGKRVKXFTL 203
121 IRENIPILG.PALDSATITLTFYNNANSAASALMWLIQSTSEAAKYKTEBOQIGKRVKXFTL 180
DB 204 PSIAITISLNSWSALSKQIQIASTNNGQFESPVLINAQNRVTITNVDAVGTSTNIAL 263
181 PSIAITISLNSWSALSKQIQIASTNNGQFESPVLINAQNRVTITNVDAVGTSTNIAL 240
QY 264 LNRNNMAAMD-DVPMTOGF 282
241 LNRNNMAAMD-DVPMTOGF 260
DB

RESULT 11
US-10-717-243-7
Sequence 7, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,651
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11092US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
TOPOLOGY: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-717-243-7

Query Match      56.8%; Score 813.5; DB 17; Length 263;
Best Local Similarity 63.8%; Pred. No. 7.2e-70;
Matches 166; Conservative 38; Mismatches 55; Indels 1; Gaps 1

QY      24 DVSFPLSGATSSSYGVFTSNLRKALPNRKKLYDILRSLSPGSGRYALHLYTNVADETI 83
DB      1 DVSFPLSGADPRSYCMFKIDLRNALPFREKYNINPLLPVSAGAGRYLLIMHLFNNYDGKTI 60
QY      84 SVAIDVTNVIYMGYAGDTSYFPFNESAATEAKYVFKDAMRKVTLPYSGNVERLQTAAGK 143
DB      61 TVAVDVTVNYIMGYLADTTSYFPNPAALAQYFRDARRKITTLPYSGNVERLQTAAGK 120
QY      144 IRENIPGLPALDSAITTLFPYNNANSASALMWLIQSTSEARVYKFIQOIGKVDKFTL 203
DB      121 PREKIPGLPALDSAISTLHYDSTFAAGALLVLIQTTEAARFKYIEGOIGERAVRDEV 180
QY      204 PSLAITSLENGSALSQIQIQLASTNNQGPRESVVLINMQNQVTTITNVDAQVYTSNIALL 263
DB      181 PSLAITSLENGSGLSKQIQIQLAQGNNGIFRTPDIVLDNKGNRVQITNVTSKVTISNIQILL 240
QY      264 LNRNNMAAMD-DVPMTOSF 282
DB      241 LNRNIAEGDNGDVSTTHGF 260

RESULT 12
US-10-127-890-5
Sequence 5, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Strudnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

```

```

1  NUMBER OF SEQUENCES: 173
2  PROTEINS
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE: McAndrews, Held & Malloy, Ltd.
5  STREET: 500 West Madison Street, 34th floor
6  CITY: Chicago
7  STATE: Illinois
8  COUNTRY: USA
9  ZIP: 60661
10
11  COMPUTER READABLE FORM:
12  MEDIUM TYPE: floppy disk
13  COMPUTER: IBM PC compatible
14  OPERATING SYSTEM: PC-DOS/MS-DOS
15  SOFTWARE: Patent In Release #1.0, Version #1.25
16
17  CURRENT APPLICATION DATA:
18  APPLICATION NUMBER: US/10/127,890
19  FILING DATE: 23-Apr-2002
20  CLASSIFICATION: <Unknown>
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22  PRIOR APPLICATION DATA:
23  APPLICATION NUMBER: US/08/646,360
24  FILING DATE: 13-MAY-1996
25  APPLICATION NUMBER: PCT/US94/05348
26  FILING DATE: 12-MAY-1994
27  APPLICATION NUMBER: US 08/064,691
28  FILING DATE: 12-MAY-1993
29  APPLICATION NUMBER: US 07/968,430
30  FILING DATE: 09-DEC-1992
31  APPLICATION NUMBER: US 07/901,707
32  FILING DATE: 19-JUN-1992
33  APPLICATION NUMBER: US 07/787,567
34  FILING DATE: 04-NOV-1991
35
36  ATTORNEY/AGENT INFORMATION:
37  NAME: McNicholas, Janet M.
38  REGISTRATION NUMBER: 32,918
39  REFERENCE/DOCKET NUMBER: 200-70.P4
40
41  TELECOMMUNICATION INFORMATION:
42  TELEPHONE: 312/707-8889
43  TELEFAX: 312/707-9155
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45  TELE: 650 388-1248
46
47  INFORMATION FOR SEQ ID NO: 5:
48
49  SEQUENCE CHARACTERISTICS:
50
51  LENGTH: 248 amino acids
52  TYPE: amino acid
53  TOPOLOGY: linear
54
55  MOLECULE TYPE: protein
56
57  SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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RESULT 13
US-10-717-243-5
; Sequence 5, Application US/10717243
; Publication No. US20050054835A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/717,243
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-717-243-5
Query Match 50.6%; Score 724.5; DB 17; Length 248;
Best Local Similarity 59.0%; Pred. No. 2.5e-61;
Matches 147; Conservative 49; Mismatches 50; Indels 3; Gaps 3;
QY 24 DVSFRLSGATSSSYGVFISNLKRALPNERKLYIPILRSSLPQSORYALIHLTNYADETI 83
DB 1 DVAFSLSSGSSSTYSKFIQDLKRALPSNGVYVNLITLLSSASGASRYTTLTSLNYDGKAI 60
QY 84 SVAIDVTNYIMYIGRAGDTSYFENEASATEAKYVFPDARKYTLPLYSNGVERLQTAAGK 143
DB 61 TYAADVDSQIXIMYILVNSTSYFNEBDAKLASQYVFKGS-TYITLFSNGYERKQTAAGK 119
QY 144 IRENIPILGLPDAISAITTLFFYNNANSAASALMWLIQSTSEBAARYKEIEQIGKRVDTPL 203
DB 120 IREKPIGLPDAISAITTLFIHYDSTAAAFVLVILQTAASRFKYTEGQILIRISKNGV 179

QY 204 PSIAISLENS-WSALSQIOIASTNNGQFESPVVLINAQNRVITTNVAGVTSNIAL 262
DB 180 PSIAISLENSLSALSQIOIAQNTNGFTKTPVITTDKQKRVETITNTSKVTATQIQ 239
QY 263 LSN-RNNMA 270
DB 240 LSNYKQNV 248
RESULT 14
US-10-127-890-4
; Sequence 4, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-127-890-4
Query Match 49.5%; Score 709; DB 14; Length 263;
Best Local Similarity 61.6%; Pred. No. 8.5e-60;
Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;
QY 24 DVSFRLSGATSSSYGVFISNLKRALPNERKLYIPILRSSLPQSORYALIHLTNYADETI 83
DB 1 DVNFDLSTATATYTKFIEDFRATLPFSHKYVDIPLYTITSDSRFLDLTSTAYERTI 60

```

QY      84  SVAIDVTNVIYMGYRAGDTSYFENEASATEAKYVKDMRKVTLTPYSGNYERLQTAAG 143
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  SVAIDVTNVIYVAYRTRDVSYPFKE-SPEAVNILEK-GTRKITLPTGNYENLQTAARK 118
QY      144  IRENIPLGIPALDSATITLFFYNNANSAALMWLIQSTSEARFYKEIQIGKRDVKTPL 203
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      119  IRENIDGLPALSSAITTLFFYNAQSPALVLQTTAEARFKYIERHVAKYVATNFK 178
QY      204  PSLAIISENSWSALSQIQIASTNNGQESPVVLINQNRVTITNVDAVTSNIALL 263
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      179  PHLAIISENSWSALSQIIFLAQNGGKFRNPVDLIKPTGERFQVTNVDSVVKGNITKL 238
QY      264  LN 265
      ||
Db      239  LN 240

RESULT 15
US-10-717-243-4
; Sequence 4, Application US/10717243
; Publication No. US20050054693A1
; GENERAL INFORMATION:
;   APPLICANT: Bectel, Marc D.
;             Carroli, Stephen F.
;             Studnika, Gary M.
;   TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                       Proteins
;   NUMBER OF SEQUENCES: 169
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;     STREET: 500 West Madison Street, 34th floor
;     CITY: Chicago
;     STATE: Illinois
;     COUNTRY: USA
;     ZIP: 60661
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Patent Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/717,243
;     FILING DATE: 18-NOV-2003
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/839,765
;     FILING DATE: 15-APR-1997
;     APPLICATION NUMBER: US 08/425,336
;     FILING DATE: 18-APR-1995
;     APPLICATION NUMBER: US 08/064,691
;     FILING DATE: 12-MAY-1993
;     APPLICATION NUMBER: US 07/988,430
;     FILING DATE: 09-DEC-1992
;     APPLICATION NUMBER: US 07/901,707
;     FILING DATE: 19-JUN-1992
;     APPLICATION NUMBER: US 07/787,567
;     FILING DATE: 04-NOV-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: McNicholas, Janet M.
;     REGISTRATION NUMBER: 32,918
;     REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 312/707-8889
;     TELEFAX: 312/707-9155
;     TELEK: 650 388-1248
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 263 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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US-10-717-243-4
Query Match          49.5%; Score 709; DB 17; Length 263;
Best Local Similarity 61.6%; Pred. No. 8,5e-60;
Matches 149; Conservative 30; Mismatches 61; Indels 2; Gaps 2;

QY      24  DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPGQRYALIHLYNVADETI 83
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  DVNFDLSTATAKTATYKTFIEDFRATLPSHKYVDIFLSTISDSRFLILDITSYAYETI 60
QY      84  SVAIDVTNVIYMGYRAGDTSYFENEASATEAKYVKDMRKVTLTPYSGNYERLQTAAG 143
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  SVAIDVTNVIYVAYRTRDVSYPFKE-SPEAVNILEK-GTRKITLPTGNYENLQTAARK 118
QY      144  IRENIPLGIPALDSATITLFFYNNANSAALMWLIQSTSEARFYKEIQIGKRDVKTPL 203
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      119  IRENIDGLPALSSAITTLFFYNAQSPALVLQTTAEARFKYIERHVAKYVATNFK 178
QY      204  PSLAIISENSWSALSQIQIASTNNGQESPVVLINQNRVTITNVDAVTSNIALL 263
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      179  PHLAIISENSWSALSQIIFLAQNGGKFRNPVDLIKPTGERFQVTNVDSVVKGNITKL 238
QY      264  LN 265
      ||
Db      239  LN 240

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Search completed: April 12, 2005, 15:31:52
 Job time : 96.4347 secs

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OM protein - protein search, using sw model

Run on: April 12, 2005, 14:53:56 ; Search time 130.481 Seconds

(without alignments)
856.626 Million cell updates/sec

Title: US-09-905-247A-1

Perfect score: 1431
Sequence: 1 MRRFLVLSLILFLITPA.....AAMDVPMQSRGCSYAL 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.16Dec04:*

1: _geneseqp1980s:*
2: _geneseqp1990s:*
3: _geneseqp2000s:*
4: _geneseqp2001s:*
5: _geneseqp2002s:*
6: _geneseqp2003as:*
7: _geneseqp2003bs:*
8: _geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1431	100.0	289	5	ABB07660
2	1429	99.9	289	4	AAB99329
3	1420	99.2	289	2	AAR07514
4	1420	99.2	289	2	AAR25572
5	1420	99.2	289	2	AAR29272
6	1420	99.2	289	2	AAR55129
7	1420	99.2	289	2	AAM10468
8	1420	99.2	289	2	AAM11870
9	1420	99.2	289	2	AAY01374
10	1420	99.2	289	3	AAM84192
11	1420	99.2	289	3	AAY87791
12	1420	99.2	289	7	ADH44106
13	1420	99.2	289	8	ADH44106
14	1417	99.0	289	2	AAR32986
15	1333	93.2	289	2	AAR07523
16	1333	93.2	289	2	AAR29276
17	1328	92.8	267	2	AAM21703
18	1328	92.8	267	2	AAM25140
19	1321	85.3	247	3	AAY69048
20	1321	85.3	248	2	AAR07518
21	1221	85.3	248	2	AAR25573
22	1218	85.1	247	2	AAR67359
23	1190	83.2	247	2	AAR21605
24	1171.5	81.9	290	2	AAR32481
25	1151	80.4	255	2	AAR74181

26	1146	80.1	246	2	AAR52636	AAR52636 Bioactive
27	1137	79.5	255	2	AAR37295	Aar37295 Plant typ
28	1137	79.5	255	2	AAR3907	Aar3907 Type I ri
29	1096.5	76.6	267	3	AAB01299	Aab01299 Wild type
30	1096.5	76.6	267	8	AD105683	Ad105683 Bryonia d
31	1081	75.5	496	4	AAB36828	Aab36828 BDI-G28.5
32	1071	74.8	247	3	AAY69043	Aay69043 Amino aci
33	1071	74.8	248	4	AAB36824	Aab36824 Residues
34	1069.5	74.7	267	3	AAB01300	Aab01300 Altered b
35	911.5	63.7	267	8	AD105689	Ad105689 Bryonia d
36	813.5	56.8	263	2	AAR63908	Aar63908 Type I ri
37	813.5	56.8	263	2	AAR74182	Aar74182 Type I ri
38	809.5	56.6	277	2	AAR29909	Aar29909 Prod. of
39	806.5	56.4	263	2	AAR37296	Aar37296 Plant typ
40	805	56.3	280	2	AAR07520	Aar07520 Alpha-Tri
41	805	56.3	280	2	AAR07521	Aar07521 Alpha-Tri
42	805	56.3	280	2	AAR25575	Aar25575 Ribosome
43	805	56.3	280	2	AAR25576	Aar25576 Ribosome
44	793.5	55.5	272	2	AAR07522	Aar07522 Alpha-Tri
45	793.5	55.5	272	2	AAR25577	Aar25577 Ribosome

ALIGNMENTS

RESULT 1	ABB07660	standard; protein; 289 AA.
ID	ABB07660	
XX	ABB07660	
AC	ABB07660	
XX	ABB07660	
DT	20-MAY-2002	(first entry)
XX	Native trichosanthin (TCS) protein sequence.	
DE	Native trichosanthin (TCS) protein sequence.	
XX	Trichosanthin; TCS; mutant; MTCS; therapeutic; cytostatic; antitumour;	
KW	anti-human immunodeficiency virus; virucide; immunostimulant; gene;	
KW	ectopic pregnancy.	
XX	Trichosanthes kirilowii.	
OS	Trichosanthes kirilowii.	
XX	Key	Location/Qualifiers
FT	Peptide	1..23
FT	Misc-difference	/note= "signal peptide"
FT	Protein	24..289
FT	Region	/note= "mature protein"
FT	Misc-difference	175
FT	Region	/note= "MTCS contains a modification of at least one amino acid residue in this region"
FT	Region	203..226
FT	Region	/note= "encoded by ATT"
FT	Region	/note= "MTCS contains a modification of at least one amino acid residue in this region"
FT	Region	230..244
FT	Misc-difference	/note= "MTCS contains a modification of at least one amino acid residue in this region"
FT	Misc-difference	289
FT	Misc-difference	/note= "encode dby ATT"
PN	WO200212537-A2.	
PD	14-FEB-2002.	
XX	18-JUL-2001; 2001MO-CN001178.	
PF	02-AUG-2000; 2000CN-00119553.	
PR	18-JAN-2001; 2001CN-00103102.	
XX	(BEIJ-) BEIJING STM BIOTECH LTD.	
PA	(KEYV/) KE Y.	

PA (NIEH/) NIE H.
 XX
 XX Ke Y, Nie H;
 XX
 XX MPI, 2002-227165/28.
 DR N-PSDB; ABA95171.
 XX
 XX Mutant trichosanthin protein of low antigenicity useful for treating
 PT tumor e.g. leukemia, comprises a sequence of native trichosanthin with
 PT modification of at least one amino acid residue in three specific
 PT regions.
 XX
 XX Example 1; Fig 1; 42pp; English.
 PS
 XX
 XX The invention relates to a mutant trichosanthin (MTCS) protein of low
 CC antigenicity comprising a sequence of native TCS with the modification of
 CC at least one amino acid residue in three regions which is 174-180, 203-
 CC 227 and 230-244 and substantially retaining the biological activities of
 CC the native TCS. The MTCS protein, its fragment or derivative is useful as
 CC an therapeutic agent; or for preparing a medicament for treating viral
 CC disease e.g. acquired immunodeficiency syndrome (AIDS), tumour e.g.
 CC leukemia, for inducing abortion and/or treating ectopic pregnancy. The
 CC present sequence represents the native TCS
 XX
 XX Sequence 289 AA;
 SQ

Query Match 100.0%; Score 1431; DB 5; Length 289;
 Best Local Similarity 100.0%; Pred. No. 1.1e-127;
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIRFLVSLILITLFLTPAVGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
 DB 1 MIRFLVSLILITLFLTPAVGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
 QY 61 RSLPSQRYALIHNTYADETISVAIDVTNYIMGRAGDTSYFNEASATEAAKYVK 120
 DB 61 RSLPSQRYALIHNTYADETISVAIDVTNYIMGRAGDTSYFNEASATEAAKYVK 120
 QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTLFYNNANSAASALMWLIQS 180
 DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTLFYNNANSAASALMWLIQS 180
 QY 181 TSEARXYKEIEQIGKRVDTKFLPSLAISLENSWSALSKQIQIASTNNGQFESPVLIN 240
 DB 181 TSEARXYKEIEQIGKRVDTKFLPSLAISLENSWSALSKQIQIASTNNGQFESPVLIN 240
 QY 241 AONORVTITNDAGVVTNSIALILNRNNMAAMDDVPMTQSFQCGSYAL 289
 DB 241 AONORVTITNDAGVVTNSIALILNRNNMAAMDDVPMTQSFQCGSYAL 289

RESULT 2
 AAB99329
 ID AAB99329 standard; protein; 289 AA.
 XX
 XX AAB99329;
 AC
 XX
 XX 23-AUG-2001 (first entry)
 DT
 XX Trichosanthes kirilowii trichosanthin (TCS) protein sequence.
 DE
 XX Trichosanthes kirilowii; trichosanthin; TCS; mutagenesis; mutation; MTCS;
 KW mutant of trichosanthin; Mongolian snake-gourd; bioactivity; selectivity;
 KM cancer; virus; HIV; metaphase induced labour.
 OS Trichosanthes kirilowii.
 XX
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 230
 FT /note= "encoded by GCA"
 FT
 XX CN1283630-A.
 XX

PD 14-FEB-2001.
 XX
 XX 02-AUG-2000; 2000CN-00119553.
 PF
 XX
 XX 02-AUG-2000; 2000CN-00119553.
 XX
 XX (SHAN-) SHANGHAI INST CYTOBIOLOGY CHINESE ACAD.
 PA
 XX Ke Y, Nie H;
 XX
 XX MPI, 2001-291745/31.
 DR N-PSDB; AAR41473.
 XX
 XX Trichosanthin mutant and its preparing process.
 PT
 XX
 XX Disclosure; Page 2 (disclosure); 15pp; Chinese.
 PS
 XX
 XX The present invention describes a trichosanthin mutant which is prepared
 CC through the mutational deformation of the trichosanthin gene and using an
 CC expression system. The trichosanthin gene is isolated from Trichosanthes
 CC kirilowii (Mongolian snake-gourd). The trichosanthin mutant has several
 CC advantages including high bioactivity, high selectivity to target, and
 CC strong kill action to cancer cells, virus and HIV. It can also be used
 CC for metaphase induced labour. The present sequence represents the protein
 CC sequence of wild type trichosanthin which is given in the exemplification
 CC of the present invention
 XX
 XX Sequence 289 AA;
 SQ

Query Match 99.9%; Score 1429; DB 4; Length 289;
 Best Local Similarity 99.7%; Pred. No. 1.7e-127;
 Matches 288; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIRFLVSLILITLFLTPAVGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
 DB 1 MIRFLVSLILITLFLTPAVGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
 QY 61 RSLPSQRYALIHNTYADETISVAIDVTNYIMGRAGDTSYFNEASATEAAKYVK 120
 DB 61 RSLPSQRYALIHNTYADETISVAIDVTNYIMGRAGDTSYFNEASATEAAKYVK 120
 QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTLFYNNANSAASALMWLIQS 180
 DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTLFYNNANSAASALMWLIQS 180
 QY 181 TSEARXYKEIEQIGKRVDTKFLPSLAISLENSWSALSKQIQIASTNNGQFESPVLIN 240
 DB 181 TSEARXYKEIEQIGKRVDTKFLPSLAISLENSWSALSKQIQIASTNNGQFESPVLIN 240
 QY 241 AONORVTITNDAGVVTNSIALILNRNNMAAMDDVPMTQSFQCGSYAL 289
 DB 241 AONORVTITNDAGVVTNSIALILNRNNMAAMDDVPMTQSFQCGSYAL 289

RESULT 3
 AAR07514
 ID AAR07514 standard; protein; 289 AA.
 XX
 XX AAR07514;
 AC
 XX
 XX 06-FEB-1991 (first entry)
 DT
 XX Trichosanthin from Trichosanthes kirilowii.
 DE
 XX Trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.
 KW trichosanthin (TCS);
 KM Trichosanthes kirilowii.
 OS Trichosanthes kirilowii.
 XX
 XX
 XX Key Location/Qualifiers
 FH 1..21
 FT /label= "signal peptide"
 FT /note= "hydrophobic"
 FT
 XX

PN W09012097-A.
 XX 18-OCT-1990.
 PD 04-APR-1989; 89US-00333184.
 XX 04-APR-1989; 89US-00333184.
 PR 04-APR-1989; 89US-00333184.
 XX (GENE-) GENELABS INC.
 PA Platek M, Chow T, Fry K;
 PI WPI; 1990-334847/44.
 DR N-PSDB; AAQ06343.
 XX
 PT Recombinant trichosanthin protein - with selective inhibitory effect on
 PT viral expression in HIV infected T-cells or monocyte-macrophase.
 XX
 PS Example; Fig 4; 102pp; English.
 CC Genomic DNA was isolated from T.kirilowii leaves from Korea and a library
 CC was constructed. Clone pQ21D was identified as likely to contain a TCS-
 CC encoding sequence in its 4kb insert. The deduced amino acid sequence is
 CC identical to that of TCS purified from Cantonese T.kirilowii roots,
 CC except for 2 conservative substitutions, i.e. Thr for Ser at position
 CC 211 and Met for Thr at position 224. The Canton protein lacks the last 19
 CC C-terminal amino acid residues. See also AAQ06344-Q06351
 XX
 SQ Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1.2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFVLVSLILILFTTPAVEGDVSPRLSGATSSSGVAFISMLRRALPNERKLYDIPLL 60
 DB 1 MRFVLVSLILILFTTPAVEGDVSPRLSGATSSSGVAFISMLRRALPNERKLYDIPLL 60
 QY 61 RSLPSSQRYALILNNYADETISVAIDVTNVTIMGRAGDISYFFNEASATAKYYVK 120
 DB 61 RSLPSSQRYALILNNYADETISVAIDVTNVTIMGRAGDISYFFNEASATAKYYVK 120
 QY 121 DAMRKVTLPYSGYVERLQTPAGKIRENIPGLPALDSATITLLPYNANSAASLMTLLOS 180
 DB 121 DAMRKVTLPYSGYVERLQTPAGKIRENIPGLPALDSATITLLPYNANSAASLMTLLOS 180
 QY 181 TSEAAKYKFEQIGRVDKTFPLSLAIIISLENSWSALSKQIOIASTNNQGFEPVVLIN 240
 DB 181 TSEAAKYKFEQIGRVDKTFPLSLAIIISLENSWSALSKQIOIASTNNQGFEPVVLIN 240
 QY 241 AONQRTITNVDAVVTSNIALILNRRNNMAAMDVDVPMTQSPFCGGSYAL 289
 DB 241 AONQRTITNVDAVVTSNIALILNRRNNMAAMDVDVPMTQSPFCGGSYAL 289

RESULT 4
 AAR25572
 ID AAR25572 standard; protein; 289 AA.
 XX
 AC AAR25572;
 XX
 DT 25-MAR-2003 (revised)
 DT 13-JAN-1993 (first entry)
 XX
 DE Trichosanthin from Trichosanthes kirilowii.
 KM TCS: alpha-trichosanthin; Radix trichosanthin; abortifacient;
 KM ribosome inactivating protein; RIP; HIV-infected human T cells;
 KM human immunodeficiency virus.
 OS Trichosanthes kirilowii.
 XX
 FH Key Location/Qualifiers

FT Misc-difference 57 /note= "Leu in previously published sequence"
 FT FT
 FT Misc-difference 60 /note= "Ile in previously published sequence"
 FT FT
 FT Misc-difference 72 /note= "Ile in previously published sequence"
 FT FT
 FT Misc-difference 82. .84 /note= "region not present in previously published
 FT sequence"
 FT FT
 FT Misc-difference 92. .93 /note= "previously published sequence contained a 10
 FT amino acid insert (DAGLPNNAVL) between Val and Tyr"
 FT FT
 FT Misc-difference 143 /note= "Gly in previously published sequence"
 FT FT
 FT Misc-difference 144 /note= "Leu in previously published sequence"
 FT FT
 FT Misc-difference 196 /note= "Ser in previously published sequence"
 FT FT
 FT Misc-difference 214. .215 /note= "previously published sequence contained a Leu
 FT inserted between Ser and Trp"
 FT FT
 FT Misc-difference 216 /note= "Leu in previously published sequence"
 FT FT
 FT Misc-difference 231 /note= "Thr in previously published sequence"
 FT FT
 FT Misc-difference 234 /note= "Ser in directly sequenced TCS"
 FT FT
 FT Misc-difference 246. .266 /note= "21 amino acids not present in previously
 FT published sequence"
 FT FT
 FT Misc-difference 247 /note= "Thr in directly sequenced TCS"
 FT FT
 PN US5128460-A.
 XX
 PD 07-JUL-1992.
 XX
 PF 04-APR-1990; 90US-00504775.
 XX
 PR 04-APR-1989; 89US-00333184.
 PR 07-SEP-1989; 89US-00404326.
 XX
 PA (GENE-) GENELABS INC.
 XX
 PI Platek M, Chow TP, Fry K;
 XX
 DR WPI; 1992-249485/30.
 DR N-PSDB; AAQ26499.
 XX
 PT Nucleic acid encoding trichosanthin protein - which can be used to
 PT inactivate ribosome(s) to inhibit protein synthesis or to inhibit HIV
 PT expression.
 XX
 PS Claim 1; Fig 4; 53pp; English.
 XX
 CC Trichosanthin protein was isolated from T.kirilowii root tuber and
 CC sequenced. The amino acid sequence was used to design sets of degenerate
 CC primers (see AAQ26506-8) for PCR amplification of the TCS coding
 CC sequence. The amplified product was used as a probe to isolate TCS coding
 CC sequence from T.kirilowii genomic libraries. One clone (pQ21D) contained
 CC a 4kb insert. The amino acid sequence deduced from the pQ21D insert
 CC differed from the purified TCS sequence by conservative substitutions at
 CC two positions (see Features Table). The differences are postulated to
 CC indicate minor variations between strains; the purified TCS was obtained
 CC from the Canton region of China and the genomic DNA was obtained from
 CC T.kirilowii leaves from Korea. The amino acid sequence was also found to
 CC differ substantially from the previously published TCS sequence (Acta
 CC Chemica Sinica, 43:943, 1984 and Pure and Appl. Chem., 58(5):789, 1986).
 CC The differences are shown in the Features Table. The present sequence
 CC agrees closely with X-ray diffraction data on crystallized TCS. The 21-
 CC amino acid insert also provides greater sequence homology with a number
 CC of RIPs such as ricin A chain and abrin A chain than the previously
 CC published sequence. (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;

Best Local Similarity 99.0%; Pred. No. 1.2e-126; Mismatches 1; Indels 0; Gaps 0;

Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRPLVLSLLITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
DB 1 MIRPLVLSLLITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
QY 61 RSSLPGSQRYALIHNTNVADETSVAIDVTNVIYMGVAGDTSYFENEASATEAKYVK 120
DB 61 RSSLPGSQRYALIHNTNVADETSVAIDVTNVIYMGVAGDTSYFENEASATEAKYVK 120
QY 121 DAMRKVTLPYSGNYERLQTPAAGKIRENIPGLPALDSAITTLFYNNANSAASALMWLIQS 180
DB 121 DAMRKVTLPYSGNYERLQTPAAGKIRENIPGLPALDSAITTLFYNNANSAASALMWLIQS 180
QY 181 TSEARARYKFIHQIGKRVDTKFLPSLAISLENSWSALSQIOIASTNNQGFETPVVLIN 240
DB 181 TSEARARYKFIHQIGKRVDTKFLPSLAISLENSWSALSQIOIASTNNQGFETPVVLIN 240
QY 241 AONQRTVITNDAGVVTNSIALILNRMNMAAMDDVPMTQSFQCGSYAL 289
DB 241 AONQRTVITNDAGVVTNSIALILNRMNMAAMDDVPMTQSFQCGSYAL 289

RESULT 5

AAR29272 standard; protein; 289 AA.

AC AAR29272;

DT 25-MAR-2003 (revised)
DT 16-APR-1993 (first entry)

DE Trichosanthin protein (encoded by pq21D).

KW TCS; alpha-trichosanthin; Radix-trichosanthin; primer; inhibition;
KW viral expression; HIV; T-cell; macrophage.

OS Synthetic.

PH Key Location/Qualifiers

FT Peptide 1..23 /label= sig_peptide

FT Protein /note= "putative N-terminal extension of the mature TCS"

FT Misc-difference 24..270 /label= mat_protein

FT Misc-difference 247 /note= "plant-derived TCS has Ser at this position"

FT Protein /note= "plant-derived TCS has Thr at this position"

FT Protein /note= "putative C-terminal extension of the mature TCS"

PN US516056-A.

PD 24-NOV-1992.

PF 09-DEC-1991; 91US-00804293.

PR 04-APR-1989; 89US-0033184.

PR 07-SEP-1989; 89US-00404326.

PA (GENE-) GENELABS INC.

PI Piatak M, Chow TP;

DR WPI, 1992-414954/50.

PT Recombinant Trichosanthin protein prodn. in E. coli - for use in the
XX selective inhibition of viral expression in HIV infected cells.
XX Disclosure; Fig 4; 37pp; English.

CC The sequence is identical to that of plant-derived TCS except for two
CC conservative changes: a Thr for a Ser substitution at position 211 and a
CC Met for a Thr substitution at position 224. TCS is likely produced as a
CC secreted protein that undergoes post-translational processing at both the
CC amino and carboxy ends. The TCS coding sequence was amplified using the
CC primers of AAQ31828-30. The amplified prod. has the sequence of AAQ31827,
CC which was used as a probe. One isolate, pq21D, comprises the sequence of
CC AAQ31826. The recombinant TCS sequence may be used in the recombinant
CC prodn. of TCS. TCS can be used for the selective inhibition of viral
CC expression in HIV-infected human T-cells or macrophages. (Updated on 25-
CC MAR-2003 to correct PF field.)

XX Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;

Best Local Similarity 99.0%; Pred. No. 1.2e-126; Mismatches 1; Indels 0; Gaps 0;

Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRPLVLSLLITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
DB 1 MIRPLVLSLLITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
QY 61 RSSLPGSQRYALIHNTNVADETSVAIDVTNVIYMGVAGDTSYFENEASATEAKYVK 120
DB 61 RSSLPGSQRYALIHNTNVADETSVAIDVTNVIYMGVAGDTSYFENEASATEAKYVK 120
QY 121 DAMRKVTLPYSGNYERLQTPAAGKIRENIPGLPALDSAITTLFYNNANSAASALMWLIQS 180
DB 121 DAMRKVTLPYSGNYERLQTPAAGKIRENIPGLPALDSAITTLFYNNANSAASALMWLIQS 180
QY 181 TSEARARYKFIHQIGKRVDTKFLPSLAISLENSWSALSQIOIASTNNQGFETPVVLIN 240
DB 181 TSEARARYKFIHQIGKRVDTKFLPSLAISLENSWSALSQIOIASTNNQGFETPVVLIN 240
QY 241 AONQRTVITNDAGVVTNSIALILNRMNMAAMDDVPMTQSFQCGSYAL 289
DB 241 AONQRTVITNDAGVVTNSIALILNRMNMAAMDDVPMTQSFQCGSYAL 289

RESULT 6

AAR55129 standard; protein; 289 AA.

AC AAR55129;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 11-JAN-1995 (first entry)

DE Alpha-trichosanthin coding.

KW Virus; recombination; plant virus; alpha trichosanthin; phenotype;
KW alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus;
KW rice necrosis virus tobamovirus; gene expression; chinese cucumber.

OS Trichosanthes kirilowii.

PN US5316931-A.

PD 31-MAY-1994.

PF 31-JUL-1992; 92US-00923692.

PR 26-FEB-1988; 88US-00160766.

PR 15-JUL-1988; 88US-00219279.

PR 17-FEB-1989; 89US-00310881.

PR 05-MAY-1989; 89US-00347637.

PR 08-JUN-1989; 89US-00363138.
 PR 22-OCT-1990; 90US-00600244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.

XX (BIOS-) BIOSOURCE GENETICS CORP.

XX PA
 PI Garger SJ, Turpen AM, Grill LK, Grantham GL, Dawson WO, Denson J,
 PI Turpen TH;

DR WPI; 1994-176269/21.
 DR N-PSDB; AAQ65573.

XX PT New recombinant plant viral nucleic acid - capable of systemic infection
 PT and scable expression of non-native nucleic acid in plant host.

XX PS Example 4; Col 47-50; 44pp; English.

XX CC The alpha-trichosanthin gene may be inserted into a recombinant plant
 CC virus which can then be used to infect plants for the production of non-
 CC native products (in this case alpha-trichosanthin). Other genes which
 CC may be inserted into the virus are those which control a phenotypic
 CC trait, such as male sterility, or sequences encoding anti-sense RNA which
 CC can be useful to prevent the expression of undesired phenotypic traits.
 CC The recombinant virus is derived from a plus sense, single stranded virus
 CC selected from tobamovirus, bromo mosaic virus, rice necrosis virus or a
 CC gemini virus. (Updated on 25-MAR-2003 to correct PF field.) (Updated on
 CC 27-AUG-2003 to correct OS field.)

XX CC Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1.2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVSLILTLFTTPAVEGVSFRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
 DB 1 MIRFLVSLILTLFTTPAVEGVSFRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60

QY 61 RSSLPQSQRVYALHITNVADETISVAIDVTNVYIMGRAGDTSYFFNEASATEAAKVF 120
 DB 61 RSSLPQSQRVYALHITNVADETISVAIDVTNVYIMGRAGDTSYFFNEASATEAAKVF 120

QY 121 DAMRKVTLPYSGYVERLQTAAGKIRENIPGLPALDSATITLFFYNNASAAALMVLIO 180
 DB 121 DAMRKVTLPYSGYVERLQTAAGKIRENIPGLPALDSATITLFFYNNASAAALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVDTFLPSLAITISLENSWMSLSKOIOASTNNQFESPVLIN 240
 DB 181 TSEAAKYKFEQOIGKRVDTFLPSLAITISLENSWMSLSKOIOASTNNQFESPVLIN 240

QY 241 AQORVITITNVDAVVTNSIALLLNRNNMAAMDDVPMTOFPGCGSYAL 289
 DB 241 AQORVITITNVDAVVTNSIALLLNRNNMAAMDDVPMTOFPGCGSYAI 289

RESULT 7
 AAW10468
 ID AAW10468 standard; protein; 289 AA.
 AC AAW10468;
 XX
 DT 17-OCT-2003 (revised)
 DT 26-APR-1997 (first entry)
 XX
 DE Chinese cucumber alpha-trichosanthin.
 XX
 KW Recombinant viral nucleic acid; RNA virus; vector; tobacco mosaic virus;
 KW TMV; Chinese cucumber; alpha-trichosanthin;
 KW ribosome inactivating protein; antiviral; virucide; transgenic plant.
 XX
 OS Trichosanthes kirilowii; Maximowicz.

XX XX
 PN WO640867-A1.

XX 19-DEC-1996.

XX 06-JUN-1996; 96WO-US009299.

XX 07-JUN-1995; 95US-00483502.

XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.

XX PA
 PI Denson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM;
 PI Garger SJ, Grill LK;

XX WPI; 1997-065181/06.

XX DR N-PSDB; AAT47094.

XX PT Recombinant viral nucleic acid producing, e.g. male sterility in plants -
 PT comprises nucleic acid whose transcription is controlled by another
 PT sequence.

XX PS Example 4; Page 124-125; 149pp; English.

XX CC Chinese cucumber alpha-trichosanthin (AAW10468) is a ribosome
 CC inactivating protein of potential use in the treatment of HIV infection.
 CC Expression vector pBC152 was constructed in which the alpha-
 CC trichosanthin coding sequence (see also AAT47094) was placed under
 CC control of the promoter of the tobacco mosaic virus-U1 coat protein gene,
 CC which had been deleted. The viral nucleic acid was capable of self-
 CC replication, encapsidation and systemic spread in infected Nicotiana
 CC benthamiana plants, and directed the high-level expression of
 CC biologically active alpha-trichosanthin in plant tissues. (Updated on 17-
 CC OCT-2003 to standardise OS field)

XX CC Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 2; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1.2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVSLILTLFTTPAVEGVSFRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
 DB 1 MIRFLVSLILTLFTTPAVEGVSFRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60

QY 61 RSSLPQSQRVYALHITNVADETISVAIDVTNVYIMGRAGDTSYFFNEASATEAAKVF 120
 DB 61 RSSLPQSQRVYALHITNVADETISVAIDVTNVYIMGRAGDTSYFFNEASATEAAKVF 120

QY 121 DAMRKVTLPYSGYVERLQTAAGKIRENIPGLPALDSATITLFFYNNASAAALMVLIO 180
 DB 121 DAMRKVTLPYSGYVERLQTAAGKIRENIPGLPALDSATITLFFYNNASAAALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVDTFLPSLAITISLENSWMSLSKOIOASTNNQFESPVLIN 240
 DB 181 TSEAAKYKFEQOIGKRVDTFLPSLAITISLENSWMSLSKOIOASTNNQFESPVLIN 240

QY 241 AQORVITITNVDAVVTNSIALLLNRNNMAAMDDVPMTOFPGCGSYAL 289
 DB 241 AQORVITITNVDAVVTNSIALLLNRNNMAAMDDVPMTOFPGCGSYAI 289

RESULT 8
 AAW11870
 ID AAW11870 standard; protein; 289 AA.
 AC AAW11870;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-APR-1997 (first entry)
 XX
 DE Chinese cucumber alpha-trichosanthin.

KW Recombinant virus; alpha-haemoglobin; human; chinese cucumber;
 KW alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin;
 XX subgenomic promoter; coat protein.
 OS Cucumis sp.
 XX
 PN US5589367-A.
 XX
 PD 31-DEC-1996.
 XX
 PF 19-JAN-1994; 94US-00184237.
 XX
 PR 26-FEB-1988; 88US-00160766.
 PR 26-FEB-1988; 88US-00160771.
 PR 15-JUL-1988; 88US-00219279.
 PR 17-FEB-1989; 89US-00310881.
 PR 05-MAY-1989; 89US-00347637.
 PR 08-JUN-1989; 89US-00363138.
 PR 22-OCT-1990; 90US-00600244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.
 PR 31-JUL-1992; 92US-00923692.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Garger SJ, Turpen AM, Grill LK, Grantham GL, Donson J, Dawson WO;
 PI Turpen TH;
 XX
 DR WPI: 1997-076845/07.
 XX
 DR N-PSDB; AAT61376.
 XX
 PT Recombinant viral DNA for altering plant phenotype or protein prodn -
 PT contains non-native sub-genomic promoter for expression of heterologous
 PT protein and native promoter for expression of coat protein.
 XX
 PS Example 4; Col 45-46; 42pp; English.
 XX
 CC The sequences given in AAM1868-71 represent proteins which were produced
 CC by the recombinant viruses of the invention. The viruses are recombinant
 CC plant viruses which comprise a native plant virus subgenomic promoter, at
 CC least one non-native plant virus subgenomic promoter, and a sequence
 CC encoding a plant virus coat protein. These heterologous sequences are
 CC preferably under the control of the native promoter sequence. By using a
 CC plant virus existing cells can be altered with a new coding sequences
 CC without involving germ cell. The recombinant viruses are stable and can
 CC cause systemic infection, with stable expression/transcription in plants
 CC that are hosts for the non-native part of the vector. The nucleotide
 CC sequences encoding these protein preferably integrated in plant viruses
 CC having either the O-coat protein or the UI-coat protein gene. (Updated on
 CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)
 CC
 SO Sequence 289 AA;
 Query Match 99.2%; Score 1420; DB 2; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1.2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 181 TSEAAKYKIEQIGKRVDTKFLPSLAITSLSNSWALSKOIOIASTNNGFETPVILIN 240
 QY 241 AONORVTITNDAGVYTSNIALLRNNMAAMDVPMTQSFCCSYAL 289
 |||||
 DB 241 AONORVMITNDAGVYTSNIALLRNNMAAMDVPMTQSFCCSYAL 289
 RESULT 9
 ID AAY01374
 AA AAY01374 standard; protein; 289 AA.
 XX
 AC AAY01374;
 XX
 DT 20-MAR-2003 (revised)
 DT 04-JUN-1999 (first entry)
 XX
 DE Chinese cucumber alpha-trichosanthin.
 XX
 KW Recombinant; plant virus; coat protein; systemic infection;
 KW transcription; therapeutic; chinese cucumber; alpha-trichosanthin.
 XX
 OS Cucumis sp.
 XX
 PN US5589367-A.
 XX
 PD 30-MAR-1999.
 XX
 PF 07-JUN-1995; 95US-00480432.
 XX
 PR 26-FEB-1988; 88US-00160766.
 PR 26-FEB-1988; 88US-00160771.
 PR 15-JUL-1988; 88US-00219279.
 PR 17-FEB-1989; 89US-00310881.
 PR 05-MAY-1989; 89US-00347637.
 PR 08-JUN-1989; 89US-00363138.
 PR 22-OCT-1990; 90US-00600244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.
 PR 31-JUL-1992; 92US-00923692.
 PR 19-JAN-1994; 94US-00184237.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Garger SJ, Turpen AM, Grill LK, Grantham GL, Donson J, Dawson WO;
 PI Turpen TH;
 XX
 DR WPI: 1999-243290/20.
 XX
 DR N-PSDB; AAX29143.
 XX
 PT Recombinant plant viral nucleic acid derived from a plus sense, single
 PT stranded RNA plant virus - useful for the transcription of products in a
 PT host.
 XX
 PS Example 4; Col 43-46; 46pp; English.
 XX
 CC The invention relates to a recombinant plant viral nucleic acid derived
 CC from a plus sense, single stranded RNA plant virus. The recombinant plant
 CC viral nucleic acid comprises: (a) a first plant viral subgenomic promoter
 CC that is native to the plus sense, single stranded RNA plant virus and
 CC operably joined to a first nucleic acid expression sequence; and (b) a
 CC second plant viral subgenomic promoter that is non-native and is operably
 CC joined to a second nucleic acid expression sequence; where, (i) (a) and
 CC (b) are incapable of recombination with one another, (ii) either the
 CC first or the second nucleic acid expression sequence is a plant viral
 CC coat protein coding sequence. The recombinant plant viral nucleic acid
 CC allows the transcription of products in a host, such as therapeutic and
 CC other useful polypeptides or proteins e.g. enzymes, complex biomolecules
 CC and ribozymes. It also gives the option of applying the coding sequence
 CC to the desired organism, tissue, organ or cell, is stable for the foreign
 CC coding sequences and is capable of systemic infection in the plant host.
 CC The transformation and regeneration of target organisms become
 CC unnecessary. (Updated on 20-MAR-2003 to correct PR field.)

XX Sequence 289 AA;
 SQ Query Match 99.2%; Score 1420; DB 2; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1.2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFVLVSLILTLFLTPAVEGDSFRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
 DB 1 MRFVLVSLILTLFLTPAVEGDSFRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
 QY RSSLPQSQRVALHLTNVADETISVAIDVTNVIWGYRADTSYFNEASATEAAKYVFK 120
 DB 61 RSSLPQSQRVALHLTNVADETISVAIDVTNVIWGYRADTSYFNEASATEAAKYVFK 120
 QY 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSATITLFFYNANSAASALMVLIO 180
 DB 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSATITLFFYNANSAASALMVLIO 180
 QY 181 TSEAAARYKFEQOIGKRVDTFLPSLAITISLENSWSLSKOIQIASTNNQOFETPVVLI 240
 DB 181 TSEAAARYKFEQOIGKRVDTFLPSLAITISLENSWSLSKOIQIASTNNQOFETPVVLI 240
 QY 241 AQNQRVTITNVDAVGTSTNIALILNRNNMAAMDVDVPMTOSFGCGSYAL 289
 DB 241 AQNQRVTITNVDAVGTSTNIALILNRNNMAAMDVDVPMTOSFGCGSYAL 289

RESULT 10
 AAM84192
 ID AAM84192 standard; protein; 289 AA.
 AC AAM84192;
 XX 27-AUG-2003 (revised)
 DT 01-APR-1999 (first entry)
 XX Chinese cucumber alpha-trichosanthin.
 DE Chinese cucumber; alpha-trichosanthin; plant virus;
 KW RNA plant virus promoter; systemic infection; foreign gene expression;
 KM AIDS therapeutic drug.
 OS Momordica cochinchinensis.
 XX US5866785-A.
 PN 02-FEB-1999.
 PD 07-JUN-1995; 95US-00482920.
 XX 26-FEB-1988; 88US-00160766.
 PR 26-FEB-1988; 88US-00160771.
 PR 15-JUL-1988; 88US-00219279.
 PR 17-FEB-1989; 89US-00310881.
 PR 05-MAY-1989; 89US-00347637.
 PR 08-JUN-1989; 89US-00363138.
 PR 22-OCT-1990; 90US-00600244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.
 PR 31-JUL-1992; 92US-00923692.
 PR 19-JAN-1994; 94US-00184237.
 XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 PA Garger SJ, Turpen AM, Grill LK, Grantham GL, Donson J, Dawson WO;
 PI Turpen TH;
 XX WPI; 1999-142035/12.
 DR N-PSDB; AAX03385.
 XX Recombinant plant viral vector - that is capable of systemic infection in

PT host plant and stable production of heterologous DNA useful for producing
 PT therapeutic proteins for treating e.g. AIDS.
 XX Example 4; Col 45-48; 45DP; English.
 PS The present sequence represents chinese cucumber alpha-trichosanthin. The
 XX nucleic acid sequence can be expressed in the plant viral constructs of
 CC the invention. The specification describes a recombinant plant viral
 CC nucleic acid derived from a positive (+)-sense RNA plant virus comprising
 CC a native (+)-sense RNA plant virus promoter that is linked to an
 CC expression sequence and a heterologous (+)-sense RNA plant virus promoter
 CC that is linked to an expression sequence. The promoters are incapable of
 CC recombination with each other, and one of the expression sequences
 CC encodes a plant viral coat protein while the other is optionally a
 CC heterologous coding sequence. The plant viral nucleic acid is capable of
 CC systemic infection in a host plant. The viral construct is useful for the
 CC introduction and expression of non-viral foreign genes in plants and the
 CC production of e.g. potential AIDS therapeutic drugs. (Updated on 27-AUG-
 CC 2003 to correct OS field.)

XX Sequence 289 AA;
 SQ Query Match 99.2%; Score 1420; DB 2; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1.2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFVLVSLILTLFLTPAVEGDSFRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
 DB 1 MRFVLVSLILTLFLTPAVEGDSFRLSGATSSSYGVFISMLRKALPNERKLYDIPLL 60
 QY RSSLPQSQRVALHLTNVADETISVAIDVTNVIWGYRADTSYFNEASATEAAKYVFK 120
 DB 61 RSSLPQSQRVALHLTNVADETISVAIDVTNVIWGYRADTSYFNEASATEAAKYVFK 120
 QY 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSATITLFFYNANSAASALMVLIO 180
 DB 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSATITLFFYNANSAASALMVLIO 180
 QY 181 TSEAAARYKFEQOIGKRVDTFLPSLAITISLENSWSLSKOIQIASTNNQOFETPVVLI 240
 DB 181 TSEAAARYKFEQOIGKRVDTFLPSLAITISLENSWSLSKOIQIASTNNQOFETPVVLI 240
 QY 241 AQNQRVTITNVDAVGTSTNIALILNRNNMAAMDVDVPMTOSFGCGSYAL 289
 DB 241 AQNQRVTITNVDAVGTSTNIALILNRNNMAAMDVDVPMTOSFGCGSYAL 289

RESULT 11
 AAY87791
 ID AAY87791 standard; protein; 289 AA.
 AC AAY87791;
 XX 06-AUG-2003 (revised)
 DT 24-AUG-2000 (first entry)
 XX Chinese cucumber alpha-trichosanthin protein.
 DE Chinese cucumber; alpha-trichosanthin; plant; male sterility; interleukin;
 KW Animal RNA virus; viral coat protein; plant; male sterility; interleukin;
 KW EBO; erythropoietin; CSF; colony stimulating factor; Factor VIII; hgm;
 KW human growth hormone; melanin; insulin; vaccine;
 KW stereo specific catalysts; alpha-trichosanthin.
 OS Trichosanthes kirilowii.
 XX US6054566-A.
 PN 25-APR-2000.
 PD 07-JUN-1995; 95US-00484341.
 PR 26-FEB-1988; 88US-00160766.
 PR 26-FEB-1988; 88US-00160771.

PR 15-JUL-1988; 88US-00219279.
 PR 17-FEB-1989; 89US-00310881.
 PR 05-MAY-1989; 89US-00347637.
 PR 08-JUN-1989; 89US-00363138.
 PR 22-OCT-1990; 90US-00600244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.
 PR 31-JUL-1992; 92US-00923692.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Garger SJ, Grill LK, Turpen TH, Grantham GL, Dawson WO;
 PI Turpen AM, Donson J;
 XX
 XX WPI; 2000-338510/29.
 DR N-PSDB; AAA12393.
 XX
 PT Recombinant non-retroviral nucleic acid for producing proteins such as
 PT interleukins, melanin and vaccines, comprises subgenomic promoters linked
 PT to sequences coding for viral coat protein and heterologous proteins.
 XX
 PS Example 4; Col 61-62; 50pp; English.
 XX
 CC This invention describes a novel recombinant viral nucleic acid (I) from
 CC a non-retroviral (+) sense, single stranded animal RNA virus comprising a
 CC nucleic acid sequence coding for a viral coat protein regulated by a
 CC native subgenomic promoter and other two heterologous nucleic acid
 CC sequences regulated by two other subgenomic promoters. (I) is useful for
 CC expressing foreign genes e.g. genes inducing male sterility in plants.
 CC (I) is also useful for producing proteins such as interleukins, EPO
 CC (erythropoietin), CSF (colony stimulating factor), Factor VIII, hGH
 CC (human growth hormone), melanin, insulin, vaccines etc., and enzymes that
 CC are useful for stereo specific catalysis of organic compounds. (I) is
 CC stable and transcribed systemically. The dual subgenomic promoter system
 CC reduces the frequency of recombination thus reducing regeneration of the
 CC wild type virus. This sequence represents a Chinese cucumber alpha-
 CC trichosanthin protein which is described in the method of the invention.
 CC (Updated on 06-AUG-2003 to correct OS field.)
 CC
 XX
 SQ Sequence 289 AA;
 Query Match 99.2%; Score 1420; DB 3; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1.2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MRFVLSTLITLFLTTTAVGSDVSFRLSGATSSSYGVFISLRLALPNERLYDIPPL 60
 DB 1 MRFVLSTLITLFLTTTAVGSDVSFRLSGATSSSYGVFISLRLALPNERLYDIPPL 60
 QY 61 RSLPSGSRVALIHLTNVADETISVAIDVTNVYIMGVRAGDTSYFNEASATEAAKYVK 120
 DB 61 RSLPSGSRVALIHLTNVADETISVAIDVTNVYIMGVRAGDTSYFNEASATEAAKYVK 120
 QY 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPILGLPALDSATITTLFFYVANSAAALMWLIQS 180
 DB 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPILGLPALDSATITTLFFYVANSAAALMWLIQS 180
 QY 181 TSEAAKYKIEOQIGRVKTFPLPSAIIISLENSWALSKQIOIASTNNGOFEPTVVLIN 240
 DB 181 TSEAAKYKIEOQIGRVKTFPLPSAIIISLENSWALSKQIOIASTNNGOFEPTVVLIN 240
 QY 241 AONQRTTNVDAGVVTSNIALILNNMAAMDVDVPMTOFSGCSYAI 289
 DB 241 AONQRTTNVDAGVVTSNIALILNNMAAMDVDVPMTOFSGCSYAI 289
 RESULT 12
 ADH44106
 ID ADH44106 standard; protein; 289 AA.
 XX
 AC ADH44106;
 XX

DT 25-MAR-2004 (first entry)
 XX
 DE Chinese cucumber alpha-trichosanthin.
 XX
 KW RNA; cis-acting replication; RNA plant virus; capped RNA molecule;
 KW coat gene; movement protein gene; subgenomic promoter;
 KW herbicide resistance; extreme temperature resistance; drought;
 KW osmotic stress; pests resistance; male sterility; female sterility;
 KW yield; collagenase cleavage site; Chinese cucumber; alpha-trichosanthin;
 KW enzyme; plant.
 XX
 XX Trichosanthes kirilowii.
 XX
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..23
 FT /note= "Signal peptide"
 FT Protein 24..289
 FT /note= "Mature alpha trichosanthin"
 XX
 XX US2003150019-A1.
 XX
 XX 07-AUG-2003.
 PD
 XX
 XX 24-OCT-2002; 2002US-00280679.
 PF
 XX
 PR 26-FEB-1988; 88US-00160766.
 PR 26-FEB-1988; 88US-00160771.
 PR 15-JUL-1988; 88US-00219279.
 PR 22-OCT-1990; 90US-00600244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.
 PR 31-JUL-1992; 92US-00923692.
 PR 07-JUN-1995; 95US-00484341.
 PR 24-APR-2000; 2000US-00557941.
 XX
 XX (LARG-) LARGE SCALE BIOLOGY CORP.
 PA
 PI Turpen TH, Turpen AM, Garger SJ, Grill LK, Donson J, Dawson WO;
 PI Grantham GL;
 XX
 XX WPI; 2003-897624/82.
 DR
 DR N-PSDB; ADH44105.
 XX
 PT New recombinant viral RNA molecules, useful in modifying a plant host
 PT cell, genotypically or phenotypically, e.g. male sterility or improved
 PT resistance to pests or diseases, or for producing pharmaceuticals,
 PT hormones or antibodies.
 XX
 PS Example 4; SEQ ID NO 4; 50pp; English.
 CC
 CC The invention relates to an RNA molecule (RVNA) comprising a cis-acting
 CC replication element from a positive strand RNA plant virus capable of
 CC replication in a plant cell and comprising an exogenous RNA segment
 CC capable of expressing its function in a host cell. The exogenous RNA
 CC segment is located in a region of the RNA molecule able to tolerate the
 CC segment without disrupting RNA replication in the absence of a trans-
 CC acting replication element in the host cell. Also included are a capped
 CC RNA molecule capable of infecting a host plant cell (where the capped RNA
 CC molecule: (a) comprises a cis-acting replication element derived from a
 CC positive strand RNA plant virus, has no extraneous non-viral sequences
 CC between the cap site and the 5' terminus of the viral sequence, and
 CC further comprises an exogenous RNA segment capable of expressing its
 CC function in a host cell in a region of the capped RNA molecule able to
 CC tolerate the segment without disrupting RNA replication of the capped RNA
 CC molecule in the absence of a trans-acting replication element in the host
 CC cell; or (b) has no extraneous non-viral sequences between the cap site
 CC and the 5' terminus of the viral sequence, and where the capped RNA
 CC molecule comprises the entire genome of the positive strand RNA virus,
 CC such as luteovirus, potyvirus, poliovirus, tombusvirus, tymovirus and
 CC tobamovirus, carmovirus, or sobemovirus, and an exogenous RNA segment
 CC capable of expressing its function in a host cell, where the exogenous
 CC RNA segment inserted into the genome of the positive strand RNA virus at

CC a gene site consisting of a coat gene site, a movement protein gene site,
 CC or another gene site under the control of a subgenomic promoter, which is
 CC one of at least two subgenomic promoters present in the virus), a DNA
 CC transcription vector comprising cDNA having one strand complementary to
 CC the (capped) RNA molecule cited above and methods of modifying a host
 CC cell, genotypically or phenotypically (comprising introducing into the
 CC cell the (capped) RNA molecule cited above, where the exogenous RNA
 CC segment confers a detectable trait in the host cell which modifies the
 CC host cell). The cis-acting replication element is derived from a
 CC monopartite plant virus, tobamovirus, or tobacco mosaic virus. The
 CC (capped) RNA molecules and DNA transcription vectors are useful in
 CC modifying a host cell, genotypically or phenotypically, e.g. improved
 CC tolerance to herbicides, extremes of heat or cold, drought or osmotic
 CC stress, improved resistance to pests or diseases, male or female
 CC sterility, or improved yield. The RNA molecules are also useful for
 CC transcription or expression of foreign genes in the host to produce the
 CC desired product, such as pharmaceuticals, hormones, antibiotics,
 CC pigments, or antibodies. The present sequence is encoded by the Chinese
 CC cucumber alpha-trichosanthin cDNA, which was used as the exogenous RNA in
 CC an RNAV of the invention.

CC Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 7; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1,2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLILITLFLTPPVEGDVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPPL 60
 DB 1 MIRFLVLSLILITLFLTPPVEGDVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPPL 60
 QY 61 RSSLPSSQRYALHLTNVADETSVAIDVTNVYIMGRAGDTSYFNEASATEAAKVF 120
 DB 61 RSSLPSSQRYALHLTNVADETSVAIDVTNVYIMGRAGDTSYFNEASATEAAKVF 120
 QY 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSAITLFFYNNASAAALMTVLIO 180
 DB 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSAITLFFYNNASAAALMTVLIO 180
 QY 181 TSEARAKYKFEBOQIGKRVKTFPLPSLAISLENSWSALSKQIQIASTNNQGFETPV 240
 DB 181 TSEARAKYKFEBOQIGKRVKTFPLPSLAISLENSWSALSKQIQIASTNNQGFETPV 240
 QY 241 AONORVITTVDAVGVTSNAILLNRMMAAMDDVMTQSFQGGSYAL 289
 DB 241 AONORVITTVDAVGVTSNAILLNRMMAAMDDVMTQSFQGGSYAI 289

RESULT 13

ADO43821
 ID ADO43821 standard; protein; 289 AA.

AC ADO43821;

DT 15-JUL-2004 (first entry)

XX Chinese cucumber alpha-trichosanthin.

XX recombinant viral nucleic acid; animal virus; subgenomic promoter;
 KM viral coat protein; IL-1; IL-2; IL-3; IL-4; IL-5; IL-6; IL-7; IL-8; IL-9;
 KM IL-10; IL-11; IL-12; EPO; G-CSF; GM-CSF; M-CSF; Factor VIII; Factor IX;
 KM tissue plasminogen activator; human growth hormone; neuro-polypeptide;
 KM melatonin; lipase; hormone; pharmaceutical; antibiotic; vaccine; insulin;
 KM Chinese cucumber; alpha-trichosanthin.

OS Trichosanthes kirilowii.

XX US2004049025-A1.

XX 11-MAR-2004.

XX 24-OCT-2002; 2002US-00280725.

PR 26-FEB-1988; 88US-00160766.
 PR 26-FEB-1988; 88US-00160771.
 PR 15-JUL-1988; 88US-00219279.
 PR 17-FEB-1989; 89US-00310881.
 PR 05-MAY-1989; 89US-00347637.
 PR 08-JUN-1989; 89US-00363138.
 PR 22-OCT-1990; 90US-00600244.
 PR 16-JAN-1991; 91US-00641617.
 PR 26-JUL-1991; 91US-00737899.
 PR 01-AUG-1991; 91US-00739143.
 PR 31-JUL-1992; 92US-00923692.
 PR 07-JUN-1995; 95US-00484341.
 PR 24-APR-2000; 2000US-00557941.

XX (LARG-) LARGE SCALE BIOLOGY CORP.

PI Donson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM;
 PI Garger SJ, Grill LK;

DR WPI, 2004-238515/22.

DR N-PSDB; ADO43820.

PT New recombinant viral nucleic acid derived from an animal virus having a
 PT native subgenomic promoter, useful in production of products such as
 PT interleukins, enzymes, and hormones.

PS Example 4; SEQ ID NO 4; 49pp; English.

XX The invention describes a recombinant viral nucleic acid derived from an
 CC animal virus possessing a native subgenomic promoter. The recombinant
 CC viral nucleic acid comprises a first viral sub genomic promoter; a first
 CC nucleic acid sequence that codes for a viral coat protein whose
 CC transcription is regulated by the first viral subgenomic promoter; a
 CC second viral sub genomic promoter; and a second nucleic acid sequence
 CC whose transcription is regulated by the second viral sub genomic
 CC promoter, where the first and second viral subgenomic promoters possess
 CC different nucleic acid sequences relative to each other, and the second
 CC nucleic acid sequence is upstream to the first nucleic acid sequence.
 CC Also described are: a non-human host animal infected by a viral vector
 CC comprising the recombinant viral nucleic acid; and a process for
 CC transcribing a nucleic acid sequence in a non-human host animal. The
 CC recombinant viral nucleic acid is useful in a sustained systemic
 CC transcription of nucleotide sequences within host cells and in producing
 CC gene products, e.g. IL-1-12, EPO, G-CSF, GM-CSF, M-CSF, Factor VIII,
 CC Factor IX, tissue plasminogen activator, human growth hormone, receptors,
 CC receptor antagonists, antibodies, neuro-polypeptides, melatonin, lipase,
 CC hormones, pharmaceuticals, antibiotics, vaccines and insulin within a
 CC host animal. This is the amino acid sequence of Chinese cucumber alpha-
 CC trichosanthin that can be incorporated into the recombinant viral protein
 CC of the invention.

XX Sequence 289 AA;

Query Match 99.2%; Score 1420; DB 8; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1,2e-126;
 Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLILITLFLTPPVEGDVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPPL 60
 DB 1 MIRFLVLSLILITLFLTPPVEGDVSPRLSGATSSSYGVFISNLRKALPNERKLYDIPPL 60
 QY 61 RSSLPSSQRYALHLTNVADETSVAIDVTNVYIMGRAGDTSYFNEASATEAAKVF 120
 DB 61 RSSLPSSQRYALHLTNVADETSVAIDVTNVYIMGRAGDTSYFNEASATEAAKVF 120
 QY 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSAITLFFYNNASAAALMTVLIO 180
 DB 121 DAMRKVTLPYSGNVERLQTAAGKIRENIPGLPALDSAITLFFYNNASAAALMTVLIO 180
 QY 181 TSEARAKYKFEBOQIGKRVKTFPLPSLAISLENSWSALSKQIQIASTNNQGFETPV 240
 DB 181 TSEARAKYKFEBOQIGKRVKTFPLPSLAISLENSWSALSKQIQIASTNNQGFETPV 240

QY 241 AONORVTITNVDAVGTSTNIALLLNRRNNMAADDVPMTOQFSCGSYAL 289
 DB 241 AONORVMTITNVDAVGTSTNIALLLNRRNNMAADDVPMTOQFSCGSYAL 289

RESULT 14

AA032986
 ID AAR32986 standard; protein; 289 AA.
 XX
 AC AAR32986;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 17-JUN-1993 (first entry)
 XX

DE Encodes chinese cucumber alpha-tricosanthin.

KW Recombinant products; commercial production; fermentation; biosynthesis;
 KW natural products; recombinant proteins; product expression;
 KW protein expression; expressed proteins.

OS Cucurbitaceae.

XX MO0303161-A1.

XX 18-FEB-1993.

XX 31-JUL-1992; 92MO-US006359.

XX 01-AUG-1991; 91US-00739143.

XX (DONS/) DONSON J.

XX (DAMS/) DAMSON W O.

XX (GRAN/) GRANTHAM G L.

XX (TURP/) TURPEN T H.

XX (GARG/) GARGER S J.

XX (GRIL/) GRILLE L K.

XX Donson J, Dawson MO, Grantham GL, Turpen TH, Turpen AM;

XX Garger SJ, Grille LK;

XX WPI; 1993-076518/09.

XX N-PSDB; AAQ37679.

XX Recombinant plant viral nucleic acids - used to express a prod., e.g.

XX antibody or IL-1 in a plant.

XX Example 4; Page 96; 30pp; English.

XX This sequence represents chinese cucumber alpha-tricosanthin. The coding

XX sequence is inserted into a recombinant plant viral nucleic acid which is

XX then used to express a recombinant product (in this case alpha-

XX tricosanthin) in a plant. The plant viral sequence may be from tobacco

XX mosaic, cucumber green mottle, cowpea mosaic, brome mosaic, broad bean

XX mottle, rice necrosis, geminiviruses, tomato golden mosaic, Casseva

XX latent and maize streak viruses. (Updated on 25-MAR-2003 to correct PN

XX field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-

XX 2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 289 AA;

XX Query Match

XX Best Local Similarity 99.0%; Score 1417; DB 2; Length 289;

XX Matches 285; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVLSLLITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60

DB 1 MIRFLVLSLLITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60

QY 61 RSLSPGSGRYALHLTNVADETISVAIDVTNVYIMGYRAGDTSYFENASATEAKYVFK 120

DB 61 RSLSPGSGRYALHLTNVADETISVAIDVTNVYIMGYRAGDTSYFENASATEAKYVFK 120

QY 121 DAMRKVTLPEYSGNYERLQTPAKGIRENIPLEGPALDSATITLFPYNNASASALNVLIOQ 180
 DB 121 DAMRKVTLPEYSGNYERLQTPAKGIRENIPLEGPALDSATITLFPYNNASASALNVLIOQ 180

QY 181 TSEARXYKFEQOIGKRVDTFLPSLAIISLENSWSALSKOIQIASTNNQGFESPVLIN 240
 DB 181 TSEARXYKFEQOIGKRVDTFLPSLAIISLENSWSALSKOIQIASTNNQGFETPVILN 240

QY 241 AONORVTITNVDAVGTSTNIALLLNRRNNMAADDVPMTOQFSCGSYAL 289
 DB 241 AONORVMTITNVDAVGTSTNIALLLNRRNNMAADDVPMTOQFSCGSYAL 289

RESULT 15

AA07523
 ID AAR07523 standard; protein; 289 AA.

XX AAR07523;

XX 06-FEB-1991 (first entry)

XX Alpha-Trichosanthin encoded by insert sequence from clone 12.

XX Trichosanthin (TCS); Human Immunodeficiency Virus; inhibition.

XX Trichosanthes kirilowii.

XX Key Location/Qualifiers

XX FT Region 1..23

XX FT Protein /label= signal peptide

XX FT Protein /label= alpha-TCS

XX MO09012097-A.

XX 18-OCT-1990.

XX 04-APR-1989; 89US-00333184.

XX 04-APR-1989; 89US-00333184.

XX (GENE-) GENELABS INC.

XX Platek M, Chow T, Fry K;

XX WPI; 1990-334847/44.

XX N-PSDB; AAQ06351.

XX Recombinant tri:chosanthin protein - with selective inhibitory effect on

XX viral expression in HIV infected T-cells or monocyte-macrophase.

XX Example; Fig 20; 102pp; English.

XX PQ30B was used as a probe to identify clones containing sequences coding

XX for TCS in a T.kirilowii genomic library. Five clones were eventually

XX isolated and sequenced, including clone 12. They were found to have

XX homology to the alpha-TCS coding sequence. See also AAQ06343-Q06350

XX Sequence 289 AA;

XX Query Match

XX Best Local Similarity 93.2%; Score 1333; DB 2; Length 289;

XX Matches 268; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 MIRFLVLSLLITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60

DB 1 MIRFLVLSLLITLFLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60

QY 61 RSLSPGSGRYALHLTNVADETISVAIDVTNVYIMGYRAGDTSYFENASATEAKYVFK 120

DB 61 RSLSPGSGRYALHLTNVADETISVAIDVTNVYIMGYRAGDTSYFENASATEAKYVFK 120

QY 121 DAMKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFYNNANSASALMVLIOG 180
DB 121 DAQRKVTLPYSGNVERLOTAAGKIRENIPGLPALDSAITTLFYNNANSASALMVLIOG 180
QY 181 TSEARARYKFEQOIGKRVDTFLPSLAISLENSWSALSKOIOIASTNNGQFESPVLIN 240
DB 181 MSEARARYKFEQOIGKRVDTFLPSLAISLENSWSALSKOIOIASTNNGQFETPVVLIN 240
QY 241 AQORVTITNVDAGVVTSNIALLLNRRNNMAMDDVPMQTGPGCGSYAL 289
DB 241 AQORVTITNVDAGVVTSNIALLLNRRNNMAVIDDHVPMQSPGCGSYAI 289

Search completed: April 12, 2005, 15:09:59
Job time : 133.481 secs

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OM protein - protein search, using sw model

Run on: April 12, 2005, 14:56:17 ; Search time 125.09 Seconds

(without alignments)
1183.080 Million cell updates/sec

Title: US-09-905-247A-1

Perfect score: 1431

Sequence: 1 MRFLVLSLILFLITPA.....AAMDVVPMTQSGRCSSVAL 289

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1429	99.9	289	1	RIP1 TRIKI
2	1426	99.7	289	2	Q84SV8
3	1425	99.6	289	2	Q94KE4
4	1415	98.9	289	2	Q41216
5	1384	96.7	289	1	RIPS TRIKI
6	1269	88.7	270	2	Q41611
7	1264	88.3	270	2	Q6PRG5
8	1260	88.1	270	2	Q8LPV7
9	1195	83.5	247	2	Q6BQ04
10	1187	82.9	247	2	Q9LRE3
11	1171.5	81.9	290	1	RIP1 BRDYI
12	866.5	60.6	286	1	RIP1 LURCY
13	809.5	56.6	277	1	RIP1 LURCY
14	782	54.6	278	2	Q00980
15	764	53.4	286	1	RIP3 MOWCH
16	762	53.2	286	1	RIP2 MOWBA
17	743	51.9	286	1	RIP1 MOWBA
18	711	49.7	254	2	Q684T5
19	682.5	47.7	294	1	RIP1 TRIAN
20	680	47.5	250	1	RIP1 LURCY
21	540.5	37.8	282	1	RIP2 BRDYI
22	476.5	33.3	136	2	Q8SAD7
23	439.5	30.7	563	2	Q8GT32
24	435.5	30.4	563	2	Q945S2
25	434.5	30.4	563	1	NIGB_SAMNI
26	432.5	30.2	563	2	Q04367
27	425	29.7	541	2	Q41174
28	421	29.4	576	1	RICI RICCO
29	418.5	29.2	275	1	Q8H1Y4
30	416.5	29.1	564	2	Q9AVR2
31	415.5	29.0	136	2	Q8SAC0

32	414	28.9	580	2	Q94BW4	Q94BW4 cinanomum
33	410	28.7	580	2	Q94BW3	Q94BW3 cinanomum
34	407.5	28.5	275	2	Q84LJ1	Q84LJ1 gnostemma
35	407	28.4	581	2	Q94BW5	Q94BW5 cinanomum
36	403.5	28.2	277	2	Q8GV09	Q8GV09 gnostemma
37	403.5	28.2	549	2	Q9FV22	Q9FV22 cinanomum
38	401.5	28.1	277	2	Q84JRI	Q84JRI gnostemma
39	400.5	28.0	277	2	Q8GV11	Q8GV11 gnostemma
40	396.5	27.7	564	1	AGSL RICCO	P06750 ricinus com
41	395.5	27.6	277	2	Q8H1Y5	Q8H1Y5 gnostemma
42	393.5	27.5	136	2	Q84LJ0	Q84LJ0 cucurbita m
43	392.5	27.4	136	2	Q84LI9	Q84LI9 cucurbita m
44	388.5	27.1	277	2	Q8GV10	Q8GV10 gnostemma
45	384.5	26.9	136	2	Q8S2R5	Q8S2R5 cucurbita m

ALIGNMENTS

RESULT 1	ID	RIP1 TRIKI	STANDARD;	PRT;	289 AA.
AC	P09989;				
DT	01-MAR-1989 (Rel. 10, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Ribosome-inactivating protein alpha-trichosanthin precursor				
DE	(EC 3.2.2.22) (tRNA N-glycosidase) (Alpha-TCS).				
OS	Trichosanthes kirilowii (Mongolian snake-gourd).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	euroside I; Cucurbitales; Cucurbitaceae; Trichosanthes.				
OX	NCBI_Taxid=3677;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRATIN=Maximowicz; TISSUE=Leaf;				
RX	MEDLINE=91153657; PubMed=1999291; DOI=10.1016/0378-1119(91)90061-F;				
RA	Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;				
RT	"Cloning of trichosanthin cDNA and its expression in Escherichia				
RT	coli.";				
RL	Gene 97:267-272(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRATIN=Maximowicz; TISSUE=Leaf;				
RX	MEDLINE=90256790; PubMed=2341400;				
RA	Chow T., Feldman R.A., Lovett M., Piatek M.;				
RT	"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a				
RT	type I ribosome-inactivating protein.";				
RL	J. Biol. Chem. 265:8670-8674(1990).				
RN	[3]				
RP	SEQUENCE OF 24-270.				
RC	STRATIN=Maximowicz; TISSUE=Tuberous root;				
RX	MEDLINE=90256789; PubMed=2341399;				
RA	Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,				
RT	Wu P., Hwang K., Piatek M.;				
RT	"Primary amino acid sequence of alpha-trichosanthin and molecular				
RT	models for abrin A-chain and alpha-trichosanthin.";				
RL	J. Biol. Chem. 265:8665-8669(1990).				
RN	[4]				
RP	SEQUENCE OF 24-270.				
RC	TISSUE=Tuberous root;				
RA	Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,				
RT	Tian G.Y., Ni C.Z.;				
RT	"Scientific evaluation of Tian Hua Fen (THF): history, chemistry and				
RT	RT application.";				
RL	Pure Appl. Chem. 58:789-798(1996).				
RN	[5]				
RP	X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).				
RX	MEDLINE=94344957; PubMed=8066085;				
RA	Zhou F., Fu Z., Chen M., Lin Y., Pan K.;				
RT	"Structure of trichosanthin at 1.88-A resolution.";				
RL	Proteins 19:4-13(1994).				
RN	[6]				

RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RA MEDLINE=95344383; PubMed=7619070;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures, active-centre geometry and
 RT dephurinating mechanism of two ribosome-inactivating proteins.";
 RL Biochem.J. 309:285-298 (1995).
 CC -1- FUNCTION: Trichosanthin is an abortion-inducing protein. It is
 CC capable of inhibiting HIV-1 infection and replication. It
 CC inactivates eukaryotic 60S ribosomal subunits.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M34858; AAA34207.1; -;
 DR EMBL: J05434; AAA34206.1; -;
 DR PIR: J0566; RUTZ.
 DR PDB: 1G1U; X-ray; A=23-270.
 DR PDB: 1G1U; X-ray; A=23-270.
 DR PDB: 1J4G; X-ray; A/B/C/D=23-270.
 DR PDB: 1MRJ; X-ray; @=24-270.
 DR PDB: 1MRK; X-ray; @=24-270.
 DR PDB: 1NL1; X-ray; A=23-270.
 DR PDB: 1OD2; X-ray; A=24-270.
 DR PDB: 1TCS; X-ray; @=24-270.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP. 1
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KW 3D-structure; Antiviral; Direct protease sequencing; Hydrolyase;
 KW Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 FT PROPEP 271 289
 FT ACT SITE 183 183
 FT CONFLICT 57 60
 FT CONFLICT 82 84
 FT CONFLICT 87 87
 FT CONFLICT 92 92
 FT CONFLICT 143 144
 FT CONFLICT 196 196
 FT CONFLICT 215 216
 FT CONFLICT 231 231
 FT CONFLICT 234 234
 FT CONFLICT 246 246
 FT CONFLICT 247 247
 FT STRAND 25 28
 FT STRAND 30 31
 FT HELIX 34 46
 FT HELIX 47 47
 FT STRAND 50 54
 FT STRAND 55 56
 FT STRAND 57 60
 FT HELIX 66 69
 FT STRAND 70 76
 FT STRAND 78 79
 FT STRAND 82 88
 FT STRAND 89 92
 FT STRAND 93 99
 FT STRAND 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT HELIX 115 117
 FT TURN 120 121

Removed in mature form.
 By similarity.
 IPLL -> LPLI (in Ref. 4).
 Missing (in Ref. 4).
 I -> L (in Ref. 4).
 V -> VDAQPRNAVL (in Ref. 4).
 KI -> GL (in Ref. 4).
 K -> S (in Ref. 4).
 WS -> LWL (in Ref. 4).
 Q -> T (in Ref. 4).
 S -> T (in Ref. 2).
 Missing (in Ref. 4).
 T -> M (in Ref. 2).

FT	STRAND	124	127
FT	HELI	134	141
FT	HELI	142	142
FT	HELI	145	147
FT	HELI	150	150
FT	HELI	152	163
FT	HELI	164	165
FT	HELI	167	180
FT	HELI	181	181
FT	HELI	182	186
FT	STRAND	187	195
FT	HELI	188	195
FT	HELI	196	196
FT	STRAND	202	202
FT	HELI	206	226
FT	TURN	227	230
FT	STRAND	231	239
FT	TURN	241	242
FT	STRAND	245	250
FT	TURN	251	252
FT	HELI	254	258
FT	TURN	259	259
FT	STRAND	260	260
FT	STRAND	263	263
FT	TURN	266	268

SEQ SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;

Best Match 99.9%; Score 1429; DB 1; Length 289;
 Query Local Similarity 99.7%; Pred. No. 8.3e-104;
 Matches 288; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MIRFLVSLILITLTLTPPAVEGVSPRLSGATSSGVFISNLKALPNERKLYDIPLL	60
DB	1	MIRFLVSLILITLTLTPPAVEGVSPRLSGATSSGVFISNLKALPNERKLYDIPLL	60
QY	61	RSLSPGQRYALIHITNVADETISVAIDVTNYINGYRAGDTSYFENASATEAKYVFK	120
DB	61	RSLSPGQRYALIHITNVADETISVAIDVTNYINGYRAGDTSYFENASATEAKYVFK	120
QY	121	DMRKYVTLPSGNYVERLQTPAGKIRENTPLGIPALDSATITLFFYNNASASALMWLIQS	180
DB	121	DMRKYVTLPSGNYVERLQTPAGKIRENTPLGIPALDSATITLFFYNNASASALMWLIQS	180
QY	181	TSEARVYFIEQIKRYDKTFPLPSLAISLNSWSALSKOIQIASTNNGOFESPVLIN	240
DB	181	TSEARVYFIEQIKRYDKTFPLPSLAISLNSWSALSKOIQIASTNNGOFESPVLIN	240
QY	241	AONQRTITTVDAVVTSTNIALILNRNNMAAMDVVPTQSFQCSYAL	289
DB	241	AONQRTITTVDAVVTSTNIALILNRNNMAAMDVVPTQSFQCSYAL	289

RESULT 2
 Q84SV8
 ID Q84SV8 PRELIMINARY; PRT; 289 AA.
 AC Q84SV8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Trichosanthin.
 GN Name=TCS;
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosoid I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;
 RL Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.

DR EMBL: AY082349; AAC72728.1; -
 DR HSP: P09989; 1MRJ.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0005098; F:RNA N-glycosylase activity; IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP.
 DR PRINTS: PRO0396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 DR HydroLase: Plant defense; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 289 AA; 31690 MW; B403148E96861PA CRC64;
 Query Match 99.7%; Score 1426; DB 2; Length 289;
 Best Local Similarity 99.3%; Pred. No. 1,4e-103;
 Matches 287; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIRFLVSLILILFLTPPAVEGDVSPRLSGATSSSYGVFISNLKRALPNERKLYDIPLL 60
 DB 1 MIRFLVSLILILFLTPPAVEGDVSPRLSGATSSSYGVFISNLKRALPNERKLYDIPLL 60
 QY 61 RSSLPQSQRVALHLTNVADETISVAIDVTNVIIMGRAGDTSFFNEASATAAKYVFK 120
 DB 61 RSTLPQSQRVALHLTNVADETISVAIDVTNVIIMGRAGDTSFFNEASATAAKYVFK 120
 QY 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPGLPALDSATITLFFYNANSAASALMWLIQS 180
 DB 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPGLPALDSATITLFFYNANSAASALMWLIQS 180
 QY 181 TSBAARYKTEIQIGKRVDTFLPSLAITSLNSWSALSKQIOIASTNNGQFSPVVLN 240
 DB 181 TSBAARYKTEIQIGKRVDTFLPSLAITSLNSWSALSKQIOIASTNNGQFSPVVLN 240
 QY 241 AQNRVTITNVDAVGVTSNIALILNRNMAAMDVDVPMTOSEFCGSYAI 289
 DB 241 AQNRVTITNVDAVGVTSNIALILNRNMAAMDVDVPMTOSEFCGSYAI 289
 RESULT 3
 Q94KE4 PRELIMINARY; PRT; 289 AA.
 AC Q94KE4
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Trichosanthin precursor.
 GN Name=TCS;
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid 1; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuan H., Wang Y., An C., Chen Z.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL: AF367252; AA052860.1; -
 DR PIR: JC5032; JC5032.
 DR HSP: P09989; 1MRJ.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0005098; F:RNA N-glycosylase activity; IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP.
 DR PRINTS: PRO0396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 DR HydroLase: Plant defense; Protein synthesis inhibitor; Signal; Toxin.

FT SIGNAL 1 23 Potential.
 FT CHAIN 24 270 trichosanthin.
 SQ SEQUENCE 289 AA; 31706 MW; A6D5602549CA557 CRC64;
 Query Match 99.6%; Score 1425; DB 2; Length 289;
 Best Local Similarity 99.0%; Pred. No. 1,7e-103;
 Matches 286; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIRFLVSLILILFLTPPAVEGDVSPRLSGATSSSYGVFISNLKRALPNERKLYDIPLL 60
 DB 1 MIRFLVSLILILFLTPPAVEGDVSPRLSGATSSSYGVFISNLKRALPNERKLYDIPLL 60
 QY 61 RSSLPQSQRVALHLTNVADETISVAIDVTNVIIMGRAGDTSFFNEASATAAKYVFK 120
 DB 61 RSTLPQSQRVALHLTNVADETISVAIDVTNVIIMGRAGDTSFFNEASATAAKYVFK 120
 QY 121 DAMRKVTLPYSGNYERLQTPAGKIRENIPGLPALDSATITLFFYNANSAASALMWLIQS 180
 DB 121 DSWRKITLPYSGNYERLQTPAGKIRENIPGLPALDSATITLFFYNANSAASALMWLIQS 180
 QY 181 TSBAARYKTEIQIGKRVDTFLPSLAITSLNSWSALSKQIOIASTNNGQFSPVVLN 240
 DB 181 TSBAARYKTEIQIGKRVDTFLPSLAITSLNSWSALSKQIOIASTNNGQFSPVVLN 240
 QY 241 AQNRVTITNVDAVGVTSNIALILNRNMAAMDVDVPMTOSEFCGSYAI 289
 DB 241 AQNRVTITNVDAVGVTSNIALILNRNMAAMDVDVPMTOSEFCGSYAI 289
 RESULT 4
 Q41216 PRELIMINARY; PRT; 289 AA.
 ID Q41216
 AC Q41216
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Trichosanthin.
 GN Name=trichosanthin; Synonyms=TCS;
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid 1; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94271613; PubMed=8003348;
 RA Zheng H., Wang B., Shaw P., Yeung H.;
 RT "Cloning and DNA sequencing of the gene encoding trichosanthin."
 RL I Chuan Hsueh Pao 21:42-51(1994).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL: S70176; AA031048.1; -
 DR PIR: JC5032; JC5032.
 DR HSP: P09989; 1U4G.
 DR GO: GO:0005098; F:RNA N-glycosylase activity; IEA.
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP.
 DR PRINTS: PRO0396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 DR HydroLase: Plant defense; Protein synthesis inhibitor; Toxin.
 KW SEQUENCE 289 AA; 31650 MW; 286AC14D48BCA175 CRC64;
 Query Match 98.9%; Score 1415; DB 2; Length 289;
 Best Local Similarity 98.3%; Pred. No. 1e-102;
 Matches 284; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MIRFLVSLILILFLTPPAVEGDVSPRLSGATSSSYGVFISNLKRALPNERKLYDIPLL 60
 DB 1 MIRFLVSLILILFLTPPAVEGDVSPRLSGATSSSYGVFISNLKRALPNERKLYDIPLL 60
 QY 61 RSSLPQSQRVALHLTNVADETISVAIDVTNVIIMGRAGDTSFFNEASATAAKYVFK 120

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Db 61 RSSLPSSQRYALVHLTNVADETISVAIDVTSVYIMGVRAGDTSYFNEASATEAAKYVK 120
QY 121 DMRKVTLPYSGNVERLQTAAGKIRENIPLGIPALDSAITTLFPYNNASASALMVLIOS 180
Db 121 DMRKVTLPYSGNVERLQTAAGKIRENIPLGIPALDSAITTLFPYNNASASALMVLIOS 180
QY 181 TSEAAKYKFEQOIGKRVKTFPLSLAITSLENSWSALSQIQIASTNNGQFESPVLIN 240
Db 181 TSEAAKYKFEQOIGKRVKTFPLSLAITSLENSWSALSQIQIASTNNGQFESPVLIN 240
QY 241 AONQVTTNNVAGVVTNSIALILNNMAAMDVPMTQSFQCGSYAL 289
Db 241 AONQVTTNNVAGVVTNSIALILNNMAAMDVPMTQSFQCGSYAL 289

RESULT 5
RIPS_TRIKI STANDARD; PRT; 289 AA.
ID P24478;
AC 01-MAR-1992 (Rel. 21, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ribosome-inactivating protein karasurin precursor (EC 3.2.2.22) (rRNA
OS N-glycosidase).
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucoside I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxId=3677;
RN (1)
RN SEQUENCE FROM N.A.
RC TISSUE=Root tuber;
RX MEDLINE=97356562; PubMed=9212998;
RA Mizukami H., Iida K., Kondo T., Ogihara Y.;
RT "Cloning and bacterial expression of a gene encoding ribosome-
RT inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
RT kirilowii var. japonica.";
RL Biol. Pharm. Bull. 20:711-713 (1997).
RN (2)
RN SEQUENCE OF 24-270.
RX MEDLINE=92005921; PubMed=1914000;
RA Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
RT "The complete amino acid sequence of an abortifacient protein,
RT karasurin.";
RL Chem. Pharm. Bull. 39:1244-1249 (1991).
CC -1- FUNCTION: Abortifacient-inducing protein. It inactivates eukaryotic 60S
CC ribosomal subunits.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC Type 1 RIP subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, AB00666; BAA21786.1; -.
CC DR PIR, JCS606; JCS606.
CC DR PIR, J00393; J00393.
CC DR HSSP, P09989; IMR1.
CC DR InterPro, IPR001574; RIP.
CC DR Pfam, PF00161; RIP; 1.
CC DR PRINTS, PR00396; SHIGARICIN.
CC DR PROSITE, PS00275; SHIGA_RICIN; 1.
CC KW Antitoxin; Direct protein sequencing; Hydrolyase; Plant defense;
CC Protein synthesis inhibitor; Signal; Toxin.
CC FT SIGNAL 1 21 Potential.
CC FT CHAIN 22 270 Ribosome-inactivating protein karasurin-

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FT FT CHAIN 24 270 C.
FT FT Ribosome-inactivating protein karasurin-
FT FT A.
FT FT PROPEP 271 289 Removed in mature form.
FT FT ACT_SITE 183 183 By similarity.
SQ SEQUENCE 289 AA, 31704 MW, 883DJ3E324287B26 CRC64;

Query Match
Best Local Similarity 96.2%; Pred No. 2.8e-100;
Matches 278; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MIRPVLSLIITLPLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60
Db 1 MIRPVLFLIITLPLTPPAVEGDVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLL 60
QY 61 RSSLPSSQRYALVHLTNVADETISVAIDVTSVYIMGVRAGDTSYFNEASATEAAKYVK 120
Db 61 RSSLPSSQRYALVHLTNVADETISVAIDVTSVYIMGVRAGDTSYFNEASATEAAKYVK 120
QY 121 DMRKVTLPYSGNVERLQTAAGKIRENIPLGIPALDSAITTLFPYNNASASALMVLIOS 180
Db 121 DMRKVTLPYSGNVERLQTAAGKIRENIPLGIPALDSAITTLFPYNNASASALMVLIOS 180
QY 181 TSEAAKYKFEQOIGKRVKTFPLSLAITSLENSWSALSQIQIASTNNGQFESPVLIN 240
Db 181 TSEAAKYKFEQOIGKRVKTFPLSLAITSLENSWSALSQIQIASTNNGQFESPVLIN 240
QY 241 AONQVTTNNVAGVVTNSIALILNNMAAMDVPMTQSFQCGSYAL 289
Db 241 AONQVTTNNVAGVVTNSIALILNNMAAMDVPMTQSFQCGSYAL 289

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RESULT 6
Q41611 PRELIMINARY; PRT; 270 AA.
ID Q41611;
AC 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Trichosanthin (Fragment).
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucoside I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxId=3677;
RN (1)
RN SEQUENCE FROM N.A.
RA Bao Y., Chu R., Han J., Zhang H., Pan N., Gu X., Chen Z.;
RT "Cloning and sequencing of trichosanthin gene and its expression in
RT Escherichia coli and tobacco plant.";
RL Sci. China, Ser. B, Chem. Life Sci. 36:669-676 (0).
RN (2)
RN SEQUENCE FROM N.A.
RA Xu L.;
RL Submitted (APR-1995) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC EMBL, U25675; AAA70096.1; -.
CC DR HSSP, P09989; IMR1.
CC DR GO, GO:0016787; F:hydrolyase activity; IEA.
CC DR GO, GO:0030598; F:rRNA N-glycosylase activity; IEA.
CC DR GO, GO:0006952; P:defense response; IEA.
CC DR GO, GO:0017148; P:negative regulation of protein biosynthesis; IEA.
CC DR GO, GO:0009405; P:pachogenes; IEA.
CC DR InterPro, IPR001574; RIP.
CC DR Pfam, PF00161; RIP; 1.
CC DR PRINTS, PR00396; SHIGARICIN.
CC DR PROSITE, PS00275; SHIGA_RICIN; 1.
CC KW Antitoxin; Plant defense; Protein synthesis inhibitor; Toxin.
CC FT NON_TER 270
CC FT SEQUENCE 270 AA, 29993 MW, 3D73FB461EABE8D4 CRC64;

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Query Match 88.7%; Score 1269; DB 2; Length 270;
 Best Local Similarity 95.2%; Pred. No. 2.6e-91;
 Matches 257; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIRFLVSLILITLFLTPPAVEGVDFRLSGATSSSYGVFISNLKALPNERKLYDIPPL 60
 DB 1 MIRFLVSLILITLFLTPPAVEGVDFRLSGATSSSYGVFISNLKALPNERKLYDIPPL 60

QY 61 RSLSPGSRVYALHLTNVADETISVAIDVTNNYIMGRAGDTSYFENEASATEAAKVF 120
 DB 61 RSLSPGSRVYALHLTNVADETISVAIDVTNNYIMGRAGDTSYFENEASATEAAKVF 120

QY 121 DAKRKVTLPYSGVNERLQTAAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180
 DB 121 DAKRKVTLPYSGVNERLQTAAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVKTFPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240
 DB 181 TSEAAKYKFEQOIGKRVKTFPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240

QY 241 AONQRTITNVDAVGTSTNIALLNRMMA 270
 DB 241 AONQRTITNVDAVGTSTNIALLNRMMA 270

RESULT 7
 ID 06PRG5 PRELIMINARY; PRT; 270 AA.
 AC 06PRG5;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Trichomastelin (Fragment).
 GN Name=tcsm;
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA M.S., An C., Chen J., Wang Y., Yuan H., Chen Z.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL: AY584242; AA692579.1; -
 DR HSSP: P16094; 1AHC.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 FT NON TER 270
 SQ SEQUENCE 270 AA; 29649 MW; 5BB513B754F9B769 CRC64;

Query Match 88.3%; Score 1264; DB 2; Length 270;
 Best Local Similarity 95.6%; Pred. No. 6.4e-91;
 Matches 258; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MIRFLVSLILITLFLTPPAVEGVDFRLSGATSSSYGVFISNLKALPNERKLYDIPPL 60
 DB 1 MIRFLVSLILITLFLTPPAVEGVDFRLSGATSSSYGVFISNLKALPNERKLYDIPPL 60

QY 61 RSLSPGSRVYALHLTNVADETISVAIDVTNNYIMGRAGDTSYFENEASATEAAKVF 120
 DB 61 RSLSPGSRVYALHLTNVADETISVAIDVTNNYIMGRAGDTSYFENEASATEAAKVF 120

QY 121 DAKRKVTLPYSGVNERLQTAAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180
 DB 121 DAKRKVTLPYSGVNERLQTAAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVKTFPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240
 DB 181 TSEAAKYKFEQOIGKRVKTFPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240

QY 241 AONQRTITNVDAVGTSTNIALLNRMMA 270
 DB 241 AONQRTITNVDAVGTSTNIALLNRMMA 270

QY 121 DAKRKVTLPYSGVNERLQTAAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180
 DB 121 DAKRKVTLPYSGVNERLQTAAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVKTFPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240
 DB 181 TSEAAKYKFEQOIGKRVKTFPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240

QY 241 AONQRTITNVDAVGTSTNIALLNRMMA 270
 DB 241 AONQRTITNVDAVGTSTNIALLNRMMA 270

RESULT 8
 ID 08LPV7 PRELIMINARY; PRT; 270 AA.
 AC 08LPV7;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Trichosanthin precursor (Fragment).
 GN Name=trcs;
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC euroids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OC NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuan H., Wang Y., Liu T., An C., Chen Z.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 DR EMBL: AY082348; AA622782.1; -
 DR PIR: JCS032; JCS032.
 DR HSSP: P09989; 1MRJ.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0030598; F:rRNA N-glycosylase activity; IEA.
 DR GO: GO:0006952; P:defense response; IEA.
 DR GO: GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PRINTS: PR00396; SHIGARICIN.
 DR PROSITE: PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
 FT CHAIN 1 23
 FT NON TER 270
 SQ SEQUENCE 270 AA; 29683 MW; 531713B754F9B769 CRC64;

Query Match 88.1%; Score 1260; DB 2; Length 270;
 Best Local Similarity 95.2%; Pred. No. 1.3e-90;
 Matches 257; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 MIRFLVSLILITLFLTPPAVEGVDFRLSGATSSSYGVFISNLKALPNERKLYDIPPL 60
 DB 1 MIRFLVSLILITLFLTPPAVEGVDFRLSGATSSSYGVFISNLKALPNERKLYDIPPL 60

QY 61 RSLSPGSRVYALHLTNVADETISVAIDVTNNYIMGRAGDTSYFENEASATEAAKVF 120
 DB 61 RSLSPGSRVYALHLTNVADETISVAIDVTNNYIMGRAGDTSYFENEASATEAAKVF 120

QY 121 DAKRKVTLPYSGVNERLQTAAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180
 DB 121 DAKRKVTLPYSGVNERLQTAAGKIRENIPGLPALDSATITLTFYNNASASALMVLIO 180

QY 181 TSEAAKYKFEQOIGKRVKTFPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240
 DB 181 TSEAAKYKFEQOIGKRVKTFPLPSLAISLENSWSALSQIOIASTNNQFESSPVVLIN 240

QY 241 AONQRTITNVDAVGTSTNIALLNRMMA 270
 DB 241 AONQRTITNVDAVGTSTNIALLNRMMA 270

```

DB      241 AONQRTIANVAVGVTSTNIAFLNNMMA 270
|||||
RESULT 9
ID      Q6BB04      PRELIMINARY;      PRT;      247 AA.
OC      Q6BB04;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
GN      Trichosanthin (Fragment).
OS      Trichosanthin kirilowii (Mongolian snake-gourd).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX      NCBI_TaxID=3677;

RN      [1]
RP      SEQUENCE FROM N.A.
RA      M.S.-L., Wang Y., Li Y.-Y., Chen Z.-L., An C.-C.;
RT      "Trichosanthin kirilowii trichosanthin (TCS) mature peptide gene.";
RL      Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases
CC      -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR      EMBL; AY669811; AAT91090.1; -.
DR      GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
DR      GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR      InterPro; IPR001574; RIP.
DR      Pfam; PF00161; RIP; 1.
DR      PRINTS; PR00396; SHIGARICIN.
DR      PROSITE; PS00275; SHIGA_RICIN; 1.
KW      Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT      NON_TER
FT      CHAIN
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE      247 AA; 27172 MW; BCBA762884F89CCE CRC64;

Query Match
Best Local Similarity 83.5%; Score 1195; DB 2; Length 247;
Matches 241; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      24 DVSFPLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADDTI 83
DB      1 DVSFPLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADDTI 60
QY      84 SVAIDVTNYYIMGYRAGDTSYFENESATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 143
DB      61 SVAIDVTNYYIMGYRAGDTSYFENESATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120
QY      144 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEARARYKFIEOQIGRVDTKL 203
DB      121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEARARYKFIEOQIGRVDTKL 180
QY      204 PSIAIISLNSWSALSQIQIASTNNGQFESPVVLINQONRVITTNVAGVTSNIALL 263
DB      181 PSIAIISLNSWSALSQIQIASTNNGQFETPVVLINQONRAITNVDAVTSNIALL 240
QY      264 LNRNNMA 270
DB      241 LNRNNMA 247

RESULT 10
ID      Q9LRE3      PRELIMINARY;      PRT;      247 AA.
OC      Q9LRE3;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Trichobaklin (Fragment).
GN      Name=TBK;

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OS      Trichosanthes sp. Bac Kan 8-98.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX      NCBI_TaxID=118182;

RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=21476888; PubMed=11592913;
RA      Van Chi P., Quoc Trung H., Thuy Ha N., Chung W.I., Binh L.T.;
RT      "Characterization of trichobaklin, a type I ribosome-inactivating
RT      protein from Trichosanthes sp. Bac Kan 8-98.";
RL      Biotechnol. Appl. Biochem. 34:85-92(2001).
CC      -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC      specific adenosine on the 28S rRNA.
CC      -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
DR      EMBL; AB033324; BAA92530.1; -.
DR      HSSP; P09989; 1J4G.
DR      GO; GO:0016787; F:hydrolase activity; IEA.
DR      GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
DR      GO; GO:0006952; P:defense response; IEA.
DR      GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
DR      GO; GO:0009405; P:pathogenesis; IEA.
DR      InterPro; IPR001574; RIP.
DR      Pfam; PF00161; RIP; 1.
DR      PRINTS; PR00396; SHIGARICIN.
DR      PROSITE; PS00275; SHIGA_RICIN; 1.
KW      Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
FT      NON_TER
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE      247 AA; 27199 MW; 89811AC32892E03F CRC64;

Query Match
Best Local Similarity 82.9%; Score 1187; DB 2; Length 247;
Matches 240; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      24 DVSFPLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADDTI 83
DB      1 DVSFPLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSQRVALIHLTNVADDTI 60
QY      84 SVAIDVTNYYIMGYRAGDTSYFENESATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 143
DB      61 SVAIDVTNYYIMGYRAGDTSYFENESATEAKYVFKDAMRKVTLPYSGNYERLQTAAGK 120
QY      144 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEARARYKFIEOQIGRVDTKL 203
DB      121 IRENIPILGIPALDSATITLTFYNNANSAASALMWLIQSTSEARARYKFIEOQIGRVDTKL 180
QY      204 PSIAIISLNSWSALSQIQIASTNNGQFESPVVLINQONRVITTNVAGVTSNIALL 263
DB      181 PSIAIISLNSWSALSQIQIASTNNGQFETPVVLINQONRAITNVDAVTSNIALL 240
QY      264 LNRNNMA 270
DB      241 LNRNNMA 247

RESULT 11
ID      RIP1_BRVDI      STANDARD;      PRT;      290 AA.
AC      P33185; Q9S819;
DT      01-OCT-1993 (Rel. 27, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Ribosome-inactivating protein bryodin I precursor (EC 3.2.2.22) (rRNA
DE      N-glycosidase) (BDI).
OS      Bryonia dioica (Red bryony).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC      eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
OX      NCBI_TaxID=3652;

RN      [1]
RP      SEQUENCE FROM N.A., MUTAGENESIS OF GLU-212, AND X-RAY CRYSTALLOGRAPHY
RP      (2.1 ANGSTROMS).

```

RC TISSUE=Leaf;
 RX MEDLINE=97228081; PubMed=9115985; DOI=10.1021/bj962474+;
 RA Gwialk S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.,
 RA Siegal C.B.;
 RT "Molecular, biological, and preliminary structural analysis of
 RT recombinant bryodin 1, a ribosome-inactivating protein from the plant
 RT Bryonia dioica.";
 RL Biochemistry 36:3095-3103(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RA Siegal C.B.;
 RT "Cloning and expression of a gene encoding bryodin 1 from Bryonia
 RT dioica.";
 RL Patent number US5541110, 30-JUL-1996.
 [3]
 RP SEQUENCE OF 24-66.
 RC TISSUE=Seed;
 RX MEDLINE=89326691; PubMed=2753596;
 RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stierpe F., Soria M.,
 RA Lappi D.;
 RT "N-terminal sequence of some ribosome-inactivating proteins.";
 RL Int. J. Pept. Protein Res. 33:263-267(1989).
 [4]
 RN SEQUENCE OF 24-43.
 RC TISSUE=Root;
 RX MEDLINE=95151812; PubMed=7849072;
 RA Siegal C.B., Gwialk S.L., Chace D., Wolff E.A., Mixan B.,
 RA Margardt H.;
 RT "Characterization of ribosome-inactivating proteins isolated from
 RT Bryonia dioica and their utility as carcinoma-reactive
 RT immunocjugates.";
 RL Bioconj. Chem. 5:423-429(1994).
 CC -1- FUNCTION: Ribosome-inactivating protein of type 1, inhibits
 CC protein synthesis in animal cells.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -1- PTM: Appears to undergo proteolytic cleavage in the C-terminal to
 CC produce a shorter protein.
 CC -1- BIOTECNOLOGY: Especially useful as immunotoxin for
 CC pharmacological applications as it has low toxicity in rats and
 CC mice but is potent once inside target cells.
 CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.
 CC -----
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 CC -----
 CC EMBL; 124020; -; NOT_ANNOTATED_CDS.
 CC PIR; S16491; S16491.
 DR PDB; 1BRX; X-ray; Y/Z=23-270.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KM 3D-structure: Direct protein sequencing; Glycoprotein; Hydrolase;
 KM Multigene family; Plant defense; Protein synthesis inhibitor; Signal;
 KM Toxin.
 FT STGNAL 1 23
 FT CHAIN 24 270
 FT PROPEP 271 290
 FT ACT_SITE 183 183
 FT ACT_SITE 212 212
 FT CARBOHYD 214 214
 FT CARBOHYD 250 250
 FT MUTAGEN 212 212
 FT CONFLICT 61 65
 FT STRAND 25 28
 FT TURN 30 31

FT HELIX 34 46
 FT TURN 47 54
 FT STRAND 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 69
 FT STRAND 70 76
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 89 92
 FT STRAND 93 99
 FT TURN 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT TURN 115 117
 FT TURN 120 121
 FT STRAND 124 127
 FT HELIX 134 141
 FT TURN 142 142
 FT HELIX 145 147
 FT STRAND 150 150
 FT HELIX 152 163
 FT TURN 164 165
 FT HELIX 167 186
 FT STRAND 187 187
 FT HELIX 188 196
 FT STRAND 202 202
 FT HELIX 206 213
 FT TURN 214 214
 FT HELIX 215 225
 FT TURN 226 230
 FT STRAND 231 239
 FT TURN 241 242
 FT STRAND 245 250
 FT TURN 251 252
 FT HELIX 254 257
 FT TURN 258 259
 FT STRAND 260 260
 FT STRAND 263 263
 FT HELIX 266 268
 SQ SEQUENCE 290 AA; 31788 MW; E966CD9C031A42DB CRC64;
 Query Match 81.9%; Score 1171.5; DB 1; Length 290;
 Best Local Similarity 81.4%; Pred. No. 1,2e-83;
 Matches 226; Conservative 26; Mismatches 27; Indels 1; Gaps 1;
 QY 1 MIFPLVLSILITLFTTPAVRGDVSPRLSGATSSSYGVFISYLKALPNERKLYDIPLL 60
 DB 1 MIKLVLMILITLIFLKSFTVEGDVSFRLSGATTSYGFIKRLREALPYERKVNIPLL 60
 QY 61 RSSLPQSQRVALIHLTNVADETVSAIDVTNYIIMGYRAGDTSYFFNEASATEAARYVK 120
 DB 61 RSSISGSGYTLHLTNVADETVSAIDVTNYIIMGYLAGDVSYFFNEASATEAARFVK 120
 QY 121 DAMRKTLTPYSGVYELQTPAGKIRENIPLGIPALDSATTLFYNNANSAASLMLVLIQS 180
 DB 121 DAKKVTLPYSGVYELQTPAGKIRENIPLGIPALDSATTLFYNNANSAASLMLVLIQS 180
 QY 181 TSEPARYKFLFOQIGKRVKTFPLSPATISLENSWGLSKQIQIASTNNGQFSPVPLIN 240
 DB 181 TSESARYKFLFOQIGKRVKTFPLSPATISLENSWGLSKQIQIASTNNGQFSPVPLIN 240
 QY 241 AONQRTITNVDAVVTSNIALLNENNAAMDDVPMQ-SFGCGSYAL 289
 DB 241 GNNQVRVITNARSARVVTSNIALLNENNAIAGIEDISMTLIGRHLGYGI 290
 RESULT 12
 ID RIP1_MOMCH STANDARD; PRT; 286 AA.
 AC P16094; P24697;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 25-OCT-2004 (rel. 45, Laet annotation update)

DE Ribosome-inactivating protein momordin I precursor (EC 3.2.2.22) (rRNA

DE N-glycosylase) (Alpha-momorcharin) (Alpha-MMC).

OS Momordica charantia (Bitter melon) (Balsam pear).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucoside 1; Cucurbitales; Cucurbitaceae; Momordica.

NCBI_TaxId=3673;

[1]

RP SEQUENCE FROM N.A.

RC TISSUE=Seed;

RX MEDLINE=91159486; PubMed=2001404; DOI=10.1016/0167-4781(91)90070-3;

RA Ho W.K.K., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;

RT "Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating

RT protein.";

RL Biochim. Biophys. Acta 1088:311-314(1991).

[2]

RP SEQUENCE OF 24-38.

RC TISSUE=Seed;

RX MEDLINE=89326691; PubMed=2753596;

RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stipe F., Soria M.,

RA Lapi D.;

RT "N-terminal sequence of some ribosome-inactivating proteins.";

RL Int. J. Pept. Protein Res. 33:263-267(1989).

[3]

RP SEQUENCE OF 24-70.

RC TISSUE=Seed;

RX MEDLINE=89005108; PubMed=3262509;

RA Casellas P., Dussosoy D., Palasca A.I., Barbieri L., Guillemot J.C.,

RA Ferrara P., Bolognesi A., Cennin P., Stipe F.;

RT "Trichostatin, a ribosome-inactivating protein from the seeds of

RT Trichosanthes kirilowii Maximowicz. Purification, partial

RT characterization and use for preparation of immunotoxins.";

RL Eur. J. Biochem. 176:581-586(1988).

[4]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

RX MEDLINE=94356447; PubMed=8075985;

RA Ren J., Wang Y., Dong Y., Stuart D.I.;

RT "The N-glycosylase mechanism of ribosome-inactivating proteins implied

RT by crystal structures of alpha-momorcharin.";

RL Structure 2:7-16(1994).

[5]

RP X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).

RX MEDLINE=94192822; PubMed=8143869; DOI=10.1016/0014-5793(94)80491-5;

RA Husain J., Tickle I.J., Wood S.P.;

RT "Crystal structure of momordin, a type I ribosome inactivating protein

RT from the seeds of Momordica charantia.";

RL FEBS Lett. 342:154-158(1994).

[6]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=95344383; PubMed=7619070;

RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;

RT "Studies on crystal structures, active-centre geometry and

RT dehydrating mechanism of two ribosome-inactivating proteins.";

RL Biochem. J. 309:285-298(1995).

[7]

RP CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

RP specific adenosine on the 28S rRNA.

CC - SIMILARITY: Belongs to the ribosome-inactivating protein family.

CC Type 1 RIP subfamily.

CC -----

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CC -----

CC EMBL; X57682; CAA0869.1; -

DR PIR; S14273; RLPUG.

DR PDB; 1AH4; X-ray; @=24-269.

DR PDB; 1AHB; X-ray; @=24-269.

DR PDB; 1AHC; X-ray; @=24-269.

DR PDB; 1F8Q; X-ray; A=24-286.

DR PDB; 1MOM; X-ray; @=24-269.

DR PDB; 1MRG; X-ray; @=24-286.

DR PDB; 1MRH; X-ray; @=24-286.

DR PDB; 1MRI; X-ray; @=24-286.

DR GLYCONSULEDB; P16094; -

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA_RICIN; 1.

KM 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;

KW Plant defense; Protein synthesis inhibitor; Signal; Toxin.

FT SIGNAL 1 23

FT CHAIN 24 269

FT PROPEP 270 286

FT ACT_SITE 183 183

FT CARBOHYD 250 250

FT STRAND 25 28

FT HELIX 34 47

FT STRAND 50 54

FT TURN 55 56

FT STRAND 57 60

FT HELIX 66 69

FT STRAND 70 76

FT TURN 78 79

FT STRAND 82 88

FT TURN 89 92

FT STRAND 93 99

FT TURN 100 101

FT STRAND 102 105

FT HELIX 109 114

FT TURN 115 117

FT TURN 120 121

FT STRAND 124 127

FT HELIX 134 141

FT STRAND 145 147

FT STRAND 150 150

FT HELIX 152 162

FT TURN 163 163

FT HELIX 167 186

FT STRAND 187 187

FT HELIX 188 195

FT TURN 196 197

FT STRAND 202 202

FT HELIX 206 225

FT TURN 226 230

FT STRAND 231 238

FT TURN 240 241

FT STRAND 246 250

FT TURN 251 252

FT HELIX 254 258

FT TURN 259 259

FT STRAND 260 260

FT STRAND 263 263

FT HELIX 266 268

SQ SEQUENCE 286 AA; 31532 MW; E1B013ABEBC216CF CRC64;

Query Match 60.6%; Score 866.5; DB 1; Length 286;

Best Local Similarity 63.3%; Pred. No. 9.7e-60;

Matches 179; Conservative 40; Mismatches 63; Indels 1; Gaps 1;

QY 1 MRFPVLSILITLTLTPAVEGVSPRLSGATSSGVFTISNRKALPNRKYDIFPL 60

DB 1 MSRFVLSFLIATPLGSGIVGDSFRLSGADPRSPGFTKDLNNALPFREKYNIFPL 60

QY 61 RSSLPQSQRVALIHLTNYADETISVAIDVTWVYIMGVRAGDTSYFENEASATEAKYVFK 120

DB 61 LPSVSGAGRYLMLHFNVDKTIITVAVDVTWVYIMGVADTTSYFENPAELASQYVFR 120

QY 121 DAMRVTLTPYSGNVERLQTAAGKIRENIPGLIPALDSAITTLFPYNNANSASALMVLTIQS 180

DB 121 DARRKITLTPYSGNVERLQIAAGKPREKIPIGIPALDSAITLHLHYDSTPAAGALLVLIQT 180

QY 181 TSEARAKFEQOIGKRVDTFLPSLAIISLENSMALSQOIQIATNNQFESSPVLLN 240
 DB 181 TSEARAKFEQOIGKRVDTFLPSLAIISLENSMALSQOIQIATNNQFESSPVLLN 240
 QY 241 AONORVITTVNDAVGTSTNIALLNRMNMAAMD-DVPMTOSE 282
 DB 241 AONORVITTVNDAVGTSTNIALLNRMNMAAMD-DVPMTOSE 282
 DB 241 NKGRRVQITNVTSTKVTSTNIOQLLNTNINIAAGNDGVSTTHGF 283

RESULT 13

RIPA LUFCY

ID RIPA LUFCY STANDARD; PRT; 277 AA.

AC 000465;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE Ribosome-inactivating protein luffin-alpha precursor (EC 3.2.2.22)
 DE (tRNA N-glycosidase).
 OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
 OX NCBI_TaxID=3670;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=92288316; PubMed=1600156;
 RA Kataoka J., Habuka N., Miyano M., Masura C., Koizumi A.;
 RT "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
 inactivating protein from Luffa cylindrica."
 RL Plant Mol. Biol. 18:1199-1202(1992).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC Type 1 RIP subfamily.

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CC EMBL; X62371; CAA44229.1; -
 DR PIR; S22494; S22494.
 DR HSSP; P16094; IAHG.
 DR InterPro: IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGARICIN; 1.
 KM Antiviral; Hydrolase; Plant defense; Protein synthesis inhibitor;
 KM Signal; Toxin.
 FT SIGNAL 1 19
 FT CHAIN 20 277 Ribosome-inactivating protein luffin-
 alpha.
 FT ACT SITE 179 179 By similarity.
 SQ SEQUENCE 277 AA; 30212 MW; EAI7FC2798C25AC CRC64;

Query Match 56.6%; Score 809.5; DB 1; Length 277;
 Best Local Similarity 60.6%; Pred. No. 2.7e-55;
 Matches 168; Conservative 45; Mismatches 59; Indels 5; Gaps 3;

QY 1 MIRFLVSLILITLFLTPPAVEGVDFSLGATSSSYGVFISNLRKALPNERKLYDIP 60
 DB 1 MKRRTV---LTLAFVAASVTEADVRSLSGSSSTSKFIDGRKALPNSGTYNNITLL 57
 QY 61 RSSLPGSGORVAILHTNVADETVSAIDVTNVIYMGIRAGDTSYFENEASATEAKYVF 120
 DB 58 LSSASGASRYILMQLSNDAKAITVAIDVTNVIYMGIRAGDTSYFENEASATEAKYVF 117
 QY 121 DAMKRVTLPSYGNVRLQTAAGKIRENIPGLPALDSAITLTFYNNANSASALMVLIOG 180

DB 118 GS-TITVLPYSGNVERLQTAAGKIRENIPGLPALDSAITLTFHYDSTAAAFLVLIQT 176
 QY 181 TSEARAKFEQOIGKRVDTFLPSLAIISLENSMALSQOIQIATNNQFESSPVLLN 240
 DB 177 TSEARAKFEQOIGKRVDTFLPSLAIISLENSMALSQOIQIATNNQFESSPVLLN 236
 QY 241 AONORVITTVNDAVGTSTNIALLN-RNMMAAMDDV 276
 DB 237 DKGRVEITNVTSTKVTSTNIOQLLNTNINIAAGNDGVSTTHGF 273

RESULT 14

RIPA LUFCY

ID RIPA LUFCY PRELIMINARY; PRT; 278 AA.

AC 000980;
 DT 01-NOV-1996 (TRMBLrel. 01, Created)
 DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
 DE B-luffin.
 OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
 OX NCBI_TaxID=3670;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=92288316; PubMed=1600156;
 RA Kataoka J., Habuka N., Miyano M., Masura C., Koizumi A.;
 RT "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
 inactivating protein from Luffa cylindrica."
 RL Plant Mol. Biol. 18:1199-1202(1992).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.

CC -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
 CC EMBL; X62372; CAA44230.1; -
 DR PIR; S23519; S23519.
 DR HSSP; P22851; INIO.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
 DR GO; GO:0009405; P:patogenesis; IEA.
 DR InterPro: IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGARICIN; 1.

KM Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
 SQ SEQUENCE 278 AA; 30586 MW; 40C26576EB3F850 CRC64;

Query Match 54.6%; Score 782; DB 2; Length 278;
 Best Local Similarity 59.0%; Pred. No. 3.9e-53;
 Matches 164; Conservative 47; Mismatches 63; Indels 4; Gaps 3;

QY 1 MIRFLVSLILITLFLTPPAVEGVDFSLGATSSSYGVFISNLRKALPNERKLYDIP 59
 DB 1 MKRRTV---LTLAFVAASVTEADVRSLSGSSSTSKFIDGRKALPNSGTYNNITLL 58
 QY 60 LRSPLGSGORVAILHTNVADETVSAIDVTNVIYMGIRAGDTSYFENEASATEAKYVF 119
 DB 59 LPSASGASRYILMQLSNDAKAITVAIDVTNVIYMGIRAGDTSYFENEASATEAKYVF 118
 QY 120 KAMKRVTLPSYGNVRLQTAAGKIRENIPGLPALDSAITLTFYNNANSASALMVLIOG 179
 DB 119 KGS-TITVLPYSGNVERLQTAAGKIRENIPGLPALDSAITLTFYNNANSASALMVLIOG 177

QY 180 STSEAAKYFIEOQIGKRVDTFLPLSLAITSLENSALSJKOIQIASTNNGQESFSPVLI 239
Db 178 TTAEARFYIEQIGKRVDTFLPLSLAITSLENSALSJKOIQIASTNNGQESFSPVLI 237
QY 240 MAQNRVTITNVAGVTSNIALINRNMAADDDVP 277
Db 238 DNKGREVEIKDVNSKVATNNIKLLANKQINAFDDGIP 275

RESULT 15
RIP3 MOMCH STANDARD; PRT; 286 AA.
ID RIP3 MOMCH STANDARD; PRT; 286 AA.
AC P24817; Q41257; Q9FSH2; Q9FUV7;
DT 01-MAR-1992 (Rel. 21, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ribosome-inactivating protein beta-momorcharin precursor (EC 3.2.2.22)
DE (tRNA N-glycosidase) (MAP 30) (B-MMC).
GN Name=MAP30; Synonyms=RIP;
OS Momordica charantia (Bitter melon) (Balsam pear).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
OC NCBI_TaxID=673;
OX NCBI_TaxID=673;
RN [1]
RN SEQUENCE FROM N.A., AND FUNCTION.
RC TISSUE=Leaf;
RX MEDLINE=95394347; PubMed=7665070; DOI=10.1016/0378-1119(95)00186-A;
RA Lee-Huang S., Huang P.L., Chen H.-C., Huang P.L., Bourinbalar A.,
RA Huang H.I., Kung H.-F.;
RT "Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter
RT melon.";
RL Gene 161:151-156 (1995).
RN [2]
RN SEQUENCE FROM N.A.
RA Quanhong Y., Rihe P., Aisheng X.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE OF 23-286 FROM N.A.
RA Wei Y.-F., Cai L.-B., Zhuang W.;
RT "Cloning rip gene and identification of its resistance to Aspergillus
RT flauvs.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE OF 23-286 FROM N.A.
RA Nguyen Huy H., Nghiem Ngoc M., Dao Huy P., Le Tran B., Nong Van H.;
RT "Expression of a RIP gene from Momordica charantia in E. coli.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE OF 24-67.
RC TISSUE=Seed;
RX MEDLINE=91032105; PubMed=1699801; DOI=10.1016/0014-5793(90)80438-O;
RA Lee-Huang S., Huang P.L., Nara P.L., Chen H.-C., Kung H.-F., Huang P.,
RA Huang H.I., Huang P.L.;
RT "WAP 30: a new inhibitor of HIV-1 infection and replication.";
RL FEBS Lett. 272:12-18 (1990).
RN [6]
RN STRUCTURE BY NMR OF 24-286, AND DNA BINDING.
RX PubMed=10571185; DOI=10.1016/S0092-8674(00)81529-9;
RA Wang Y.-X., Neesmet N., Jacob J., Palmer I., Stahl S.J., Kaufman J.D.,
RA Huang P.L., Huang P.L., Winslow H.E., Pommer Y., Wingfield P.T.,
RA Lee-Huang S., Bax A., Torchia D.A.;
RT "Solution structure of anti-HIV-1 and anti-tumor protein MAP30:
RT structural insights into its multiple functions.";
RL Cell 99:433-442 (1999).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 24-272.
RX PubMed=10329776; DOI=10.1107/S090744499003297;
RA Yuan Y.-R., He Y.-N., Xiong J.-P., Xia Z.-X.;
RT "Three-dimensional structure of beta-momorcharin at 2.55 A
RT resolution.";
RL Acta Crystallogr. D 55:1144-1151 (1999).
CC -I- FUNCTION: Possesses anti-HIV and anti-tumor activities. Inh.bites

CC HIV-1 integrase, irreversibly relax supercoiled DNA and catalyzes
CC double-stranded breakage. Acts also as a ribosome inactivating
CC protein.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -I- PTM: Bound to a branched hexaaccharide.
CC -I- MISCELLANEOUS: Manganese or zinc required for enhancing substrate
CC binding rather than catalysis.
CC -I- MISCELLANEOUS: The oligosaccharide does not influence the fold of
CC the polypeptide chain and probably does not play a role in the
CC enzymatic function.
CC -I- MISCELLANEOUS: Is not toxic to uninfected normal cells as it
CC cannot enter into them.
CC -I- SIMILARITY: Belongs to the ribosome-inactivating protein family.
CC Type 1 RIP subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC or send an email to license@isb-sib.ch).
CC -----
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CC EMBL; AF284811; AAG3028.1; -;
CC EMBL; AY523412; AAS17014.1; -;
CC EMBL; AJ294541; CAC08217.1; -;
CC PIR; B61318; B61318.
CC PIR; J04235; J04235.
CC PDB; 1CF5; X-ray; A/B=-.
CC DR InterPro; IPR001574; RIP.
CC DR Pfam; PRO0161; RIP; 1.
CC DR PRINTS; PRO0336; SHICARICIN.
CC DR PROSITE; PS00275; SHIGA_RICIN; 1.
CC KW 3D-structure; Antiviral; Direct protein sequencing; Glycoprotein;
CC KM Hydrolyase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
CC FT SIGNAL 1 23
CC FT CHAIN 24 286
CC FT ACT SITE 93 93
CC FT ACT SITE 132 132
CC FT ACT SITE 181 181
CC FT ACT SITE 184 184
CC FT CARBOHYD 74 74
CC FT CONFLICT 23 23
CC FT CONFLICT 37 37
CC FT CONFLICT 67 67
CC FT CONFLICT 147 147
CC FT CONFLICT 188 188
CC FT CONFLICT 228 228
CC SQ SEQUENCE 286 AA, 32030 MM, 682DPS5A4ID8F921 CRC64;
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Best Local Similarity 59.6%; Pred. No. 1e-51;
Matches 158; Conservative 38; Mismatches 67; Indels 2; Gaps 2;
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Db 1 MWKLLSLFLAIFRIPAKGDVNFPLSTATATYKFIEDFRATLPFSHKVDIPLL 60
QY 61 RSLSGSQVYLIHLYNVADETSVAIDVTWYIMGYAGDPSPYFNEASATEAKYVK 120
Db 61 VSTISDRRFLIHLNLSYAVETISVAIDVTWYIMGYAGDPSPYFNEASATEAKYVK 119
QY 121 DAMKRVTLTPYSGNVERLQTAAGKIRENIPLGIPALDSATITLFFYNANSAPALMVLVLIQS 180
Db 120 -GTRITITLPTGNYENLQTAHAKIRENIDLGIPALSSATITLFFYNAGSAPALVLIQF 178
QY 181 TSEAAKYFIEOQIGKRVDTFLPLSLAITSLENSALSJKOIQIASTNNGQESFSPVLI 240
Db 179 TTAARFYIEHVAKYVATNFKPMLAITSLENSALSJKOIQIASTNNGQESFSPVLI 238

Wed Apr 13 09:27:10 2005

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Page 11

Qy 241 AQNORVTITNWDAGVTSNIALILN 265
Db 239 PTGERFOVTNVDSDVVKGNIKILIN 263

Search completed: April 12, 2005, 15:13:58
Job time : 127.09 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2005, 15:05:22 ; Search time 37.2034 Seconds
(without alignments)
579.883 Million cell updates/sec

Title: US-09-905-247A-1

Perfect score: 1431

Sequence: 1 MRRFLVSLILFLITPA.....AAMDVPMQSGRCSSVAL 289

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

513545

Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA:
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3: /cgn2_6/prodata/1/iaa/5B COMB pep: *
4: /cgn2_6/prodata/1/iaa/6A COMB pep: *
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6: /cgn2_6/prodata/1/iaa/6C COMB pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1420	99.2	289	1	US-07-923-692C-4
2	1420	99.2	289	1	US-08-184-237-4
3	1420	99.2	289	2	US-08-482-920-4
4	1420	99.2	289	3	US-08-484-341-4
5	1420	99.2	289	3	US-08-483-502-4
6	1420	99.2	289	4	US-09-726-651A-4
7	1328	92.8	267	1	US-08-378-761A-74
8	1328	92.8	267	1	US-08-485-286-74
9	1209	84.5	247	1	US-08-488-113B-6
10	1209	84.5	247	1	US-08-477-84B-6
11	1209	84.5	247	2	US-08-646-360-6
12	1209	84.5	247	3	US-08-839-765-6
13	1209	84.5	247	3	US-09-136-389-6
14	1209	84.5	247	3	US-09-610-838-6
15	1209	84.5	247	4	US-09-711-485-6
16	1171.5	81.9	230	1	US-08-245-754A-2
17	1171.5	81.9	230	2	US-08-597-731-2
18	1137	79.5	255	1	US-07-901-707-6
19	1137	79.5	255	1	US-07-988-430-6
20	1137	79.5	255	1	US-08-425-336-6
21	1137	79.5	255	5	PCT-US92-09487-6
22	1081	75.5	496	3	US-08-902-486-15
23	1071	74.8	248	3	US-08-902-486-7
24	813.5	56.8	263	1	US-07-901-707-7
25	813.5	56.8	263	1	US-07-988-430-7
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ALIGNMENTS

28	813.5	56.8	263	1	US-08-477-484B-7	Sequence 7, App1
29	813.5	56.8	263	2	US-08-646-360-7	Sequence 7, App1
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33	813.5	56.8	263	4	US-09-711-485-7	Sequence 7, App1
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35	764	53.4	250	1	US-08-378-761A-78	Sequence 78, App1
36	764	53.4	250	1	US-08-485-286-78	Sequence 78, App1
37	757	52.9	248	1	US-08-324-301-13	Sequence 13, App1
38	724.5	50.6	248	1	US-07-901-707-5	Sequence 5, App1
39	724.5	50.6	248	1	US-07-988-430-5	Sequence 5, App1
40	724.5	50.6	248	1	US-08-425-336-5	Sequence 5, App1
41	724.5	50.6	248	1	US-08-378-761A-75	Sequence 75, App1
42	724.5	50.6	248	1	US-08-485-286-75	Sequence 75, App1
43	724.5	50.6	248	1	US-08-488-113B-5	Sequence 5, App1
44	724.5	50.6	248	1	US-08-477-84B-5	Sequence 5, App1
45	724.5	50.6	248	2	US-08-646-360-5	Sequence 5, App1

RESULT 1
US-07-923-692C-4
Sequence 4, Application US/07923692C
Patent No. 5316931
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Gargier, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Perry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,692C
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 219,279
/ FILING DATE: 15-JUL-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Halluin, Albert P.
/ REGISTRATION NUMBER: 28,957
/ REFERENCE/DOCKET NUMBER: BIOG-20121
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-433-4150
/ TELEFAX: 415-433-8716
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 289 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-07-923-692C-4

Query Match          99.2%; Score 1420; DB 1; Length 289;
Best Local Similarity 99.0%; Pred. No. 9.3e-138;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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DB 121 DAMRKVTLPYSGNYERLQTAQKIRENIPLGIPALDSAITTLFYNNANSAASALMWLIQS 180
QY 181 TSEAAARYKIEQOIGKRVDTFLPSLAITISLENSWSALSKQIOIASTNNGQFETPVVLIN 240
DB 181 TSEAAARYKIEQOIGKRVDTFLPSLAITISLENSWSALSKQIOIASTNNGQFETPVVLIN 240
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DB 241 AQNRVMTITNVDAGVVTSNIALLNRRNMAMDDVPMTOGFGCGSYAL 289

RESULT 2
US-08-184-237-4
/ Sequence 4, Application US/08184237
/ Patent No. 5589367
/ GENERAL INFORMATION:
/ APPLICANT: Donson, Jon
/ APPLICANT: Dawson, William O.
/ APPLICANT: Grantham, George L.
/ APPLICANT: Turpen, Thomas H.
/ APPLICANT: Turpen, Ann Myers
/ APPLICANT: Gargier, Stephen J.
/ APPLICANT: Grill, Laurence K.
/ TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Limbach & Limbach
/ STREET: 2001 Ferry Building
/ CITY: San Francisco
/ STATE: CAL
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/184,237
/ FILING DATE:
/ CLASSIFICATION: 435
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 923,692
/ FILING DATE: 31-JUL-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 600,244
/ FILING DATE: 22-OCT-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 641,617
/ FILING DATE: 16-JAN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 310,881
/ FILING DATE: 17-FEB-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 160,766
/ FILING DATE: 26-FEB-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 160,771
/ FILING DATE: 26-FEB-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 347,637
/ FILING DATE: 05-MAY-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 363,138
/ FILING DATE: 08-JUN-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 219,279
/ FILING DATE: 15-JUL-1988
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Halluin, Albert P.
/ REGISTRATION NUMBER: 28,957
/ REFERENCE/DOCKET NUMBER: BIOG-20121 USA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-433-4150
/ TELEFAX: 415-433-8716
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 289 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-184-237-4

Query Match          99.2%; Score 1420; DB 1; Length 289;
Best Local Similarity 99.0%; Pred. No. 9.3e-138;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFVLVLILITLFTTPAVEGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
DB 1 MRFVLVLILITLFTTPAVEGDSFRLSGATSSSYGVFISNLKALPNERKLYDIPLL 60
QY 61 RSLPGSORVALIHLTNVADETISVAIDVTNVIYIGYRAGDTSYFNEASATEAKYVK 120
DB 61 RSLPGSORVALIHLTNVADETISVAIDVTNVIYIGYRAGDTSYFNEASATEAKYVK 120
QY 121 DAMRKVTLPYSGNYERLQTAQKIRENIPLGIPALDSAITTLFYNNANSAASALMWLIQS 180
DB 121 DAMRKVTLPYSGNYERLQTAQKIRENIPLGIPALDSAITTLFYNNANSAASALMWLIQS 180
QY 181 TSEAAARYKIEQOIGKRVDTFLPSLAITISLENSWSALSKQIOIASTNNGQFETPVVLIN 240
DB 181 TSEAAARYKIEQOIGKRVDTFLPSLAITISLENSWSALSKQIOIASTNNGQFETPVVLIN 240
QY 241 AQNRVMTITNVDAGVVTSNIALLNRRNMAMDDVPMTOGFGCGSYAL 289
DB 241 AQNRVMTITNVDAGVVTSNIALLNRRNMAMDDVPMTOGFGCGSYAL 289

RESULT 3
US-08-482-920-4
/ Sequence 4, Application US/08482920
/ Patent No. 5866785
/ GENERAL INFORMATION:
/ APPLICANT: Donson, Jon
```

APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS.
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Penite & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,920
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 184,237
FILING DATE: 19-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 8129-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-920-4
Query Match 99.2%; Score 1420; DB 2; Length 289;
Best Local Similarity 99.0%; Pred. No. 9.3e-138;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIFVLVSLILILFLITTPAVEDVSRSLGATSSSGVGVISNLRALPNERKLYDIPLL 60
DB 1 MIFVLVSLILILFLITTPAVEDVSRSLGATSSSGVGVISNLRALPNERKLYDIPLL 60
QY 61 RSSLPQSGRYALIHILTNVADETISVAIDVTNVYIMGYRADTGYFNEASATEAAKVFK 120

|||||
DB 61 RSSLPQSGRYALIHILTNVADETISVAIDVTNVYIMGYRADTGYFNEASATEAAKVFK 120
QY 121 DAMRKVTLPYSGNYEQLQTAQKIRENIPLGAPALDSATITLFFYNNANASALMWLLOS 180
DB 121 DAMRKVTLPYSGNYEQLQTAQKIRENIPLGAPALDSATITLFFYNNANASALMWLLOS 180
QY 181 TSEAAKYKFTIEQIGKRVKFTPLSLATISLNSMSALSQKQIQASTNNQFESSPVVLIN 240
DB 181 TSEAAKYKFTIEQIGKRVKFTPLSLATISLNSMSALSQKQIQASTNNQFESSPVVLIN 240
QY 241 AONQRTITNVDAVVTNSIALILNRRNNAAMDVDVPMTOQSGCGSYAL 289
DB 241 AONQRTITNVDAVVTNSIALILNRRNNAAMDVDVPMTOQSGCGSYAL 289
RESULT 4
US-08-484-341-4
Sequence 4, Application US/08484341
GENERAL INFORMATION:
APPLICANT: Donson, Jon
Dawson, William O.
Grantham, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,341
FILING DATE: 07-JUN-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,237
FILING DATE: <Unknown>
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-484-341-4

Query Match 99.2%; Score 1420; DB 3; Length 289;
Best Local Similarity 99.0%; Pred. No. 9.3e-138;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFVLVSLILITLFLTPTPAVEGDSFRLSGATSSSYGVFISLNKRALPNERKLYDIPLL 60
DB 1 MRFVLVSLILITLFLTPTPAVEGDSFRLSGATSSSYGVFISLNKRALPNERKLYDIPLL 60
QY 61 RSSLPQSQRVALIHLTNVADETISSAIDVTNVIYINGRAGDTSYFFNEASATEAKYVFK 120
DB 61 RSSLPQSQRVALIHLTNVADETISSAIDVTNVIYINGRAGDTSYFFNEASATEAKYVFK 120
QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNANSASALMWLIQS 180
DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNANSASALMWLIQS 180
QY 181 TSEAAKYFIEQIGKRVKDFLPSLAITISLENSWSLSKQIQIASTNNGQFETPVVLIN 240
DB 181 TSEAAKYFIEQIGKRVKDFLPSLAITISLENSWSLSKQIQIASTNNGQFETPVVLIN 240
QY 241 AQNQRVTITNVDAVVTSNIALILNRRNNMAAMDVPMTQSFQCGSYAL 289
DB 241 AQNQRVTITNVDAVVTSNIALILNRRNNMAAMDVPMTQSFQCGSYAL 289

RESULT 5
US-08-483-502-4
Sequence 4, Application US/08483502

GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,502
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/739,143
FILING DATE:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 18604-090574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-502-4

Query Match 99.2%; Score 1420; DB 3; Length 289;
Best Local Similarity 99.0%; Pred. No. 9.3e-138;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRFVLVSLILITLFLTPTPAVEGDSFRLSGATSSSYGVFISLNKRALPNERKLYDIPLL 60
DB 1 MRFVLVSLILITLFLTPTPAVEGDSFRLSGATSSSYGVFISLNKRALPNERKLYDIPLL 60
QY 61 RSSLPQSQRVALIHLTNVADETISSAIDVTNVIYINGRAGDTSYFFNEASATEAKYVFK 120
DB 61 RSSLPQSQRVALIHLTNVADETISSAIDVTNVIYINGRAGDTSYFFNEASATEAKYVFK 120
QY 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNANSASALMWLIQS 180
DB 121 DAMRKVTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFYNNANSASALMWLIQS 180
QY 181 TSEAAKYFIEQIGKRVKDFLPSLAITISLENSWSLSKQIQIASTNNGQFETPVVLIN 240
DB 181 TSEAAKYFIEQIGKRVKDFLPSLAITISLENSWSLSKQIQIASTNNGQFETPVVLIN 240
QY 241 AQNQRVTITNVDAVVTSNIALILNRRNNMAAMDVPMTQSFQCGSYAL 289
DB 241 AQNQRVTITNVDAVVTSNIALILNRRNNMAAMDVPMTQSFQCGSYAL 289

RESULT 6
US-09-726-651A-4
Sequence 4, Application US/09726651A

GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann M.
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
FILE REFERENCE: 008010023CNU01
CURRENT APPLICATION NUMBER: US/09/726,651A
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 08/483,502
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/184,237

PRIOR FILING DATE: 1994-01-19
PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
PRIOR APPLICATION NUMBER: 07/737,899
PRIOR FILING DATE: 1991-07-26
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 289
TYPE: PRT
ORGANISM: Chinese Cucumber alpha-trichosanthin
US-09-726-651A-4

Query Match 99.2%; Score 1420; DB 4; Length 289;
Best Local Similarity 99.0%; Pred. No. 9,3e-138;
Matches 286; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIRFLVSLIILFLTPPAVEGVDFRISGATSSSYGVFISNLKALPNERKLYDIPLL 60
DB 1 MIRFLVSLIILFLTPPAVEGVDFRISGATSSSYGVFISNLKALPNERKLYDIPLL 60
QY 61 RSSLPSSQRYALHLTNVADETSVAIDVTNNYIMGYRAGDTSYFNEASATEAKYVFK 120
DB 61 RSSLPSSQRYALHLTNVADETSVAIDVTNNYIMGYRAGDTSYFNEASATEAKYVFK 120
QY 121 DARAKTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFFYNNASASALMWLIOS 180
DB 121 DARAKTLPYSGNYERLQTAAGKIRENIPGLPALDSAITTLFFYNNASASALMWLIOS 180
QY 181 TSEAAKYFIEQIGKRVDTFPLSLAIISELSWSALSQIQIASTNNQFESPVVLIIN 240
DB 181 TSEAAKYFIEQIGKRVDTFPLSLAIISELSWSALSQIQIASTNNQFESPVVLIIN 240
QY 241 AONQRTITNVDAGVVTSNIALILNRNNMAAMDDVPMTOGFCGGSVAL 289
DB 241 AONQRTITNVDAGVVTSNIALILNRNNMAAMDDVPMTOGFCGGSVAL 289

RESULT 7
US-08-378-761A-74
Sequence 74, Application US/08378761A
Patent No. 563384
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651

REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-761A-74

Query Match 92.8%; Score 1328; DB 1; Length 267;
Best Local Similarity 99.6%; Pred. No. 2.4e-128;
Matches 266; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 GDVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPSSQRYALHLTNVADET 82
DB 1 GDVSPRLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPSSQRYALHLTNVADET 82
QY 83 ISVAIDVTNNYIMGYRAGDTSYFNEASATEAKYVFKDAMRKVTLPSGNYERLQTAAG 142
DB 61 ISVAIDVTNNYIMGYRAGDTSYFNEASATEAKYVFKDAMRKVTLPSGNYERLQTAAG 120
QY 143 KIRENIPGLPALDSAITTLFFYNNASASALMWLIOSTSEAAKYFIEQIGKRVDTF 202
DB 121 KIRENIPGLPALDSAITTLFFYNNASASALMWLIOSTSEAAKYFIEQIGKRVDTF 180
QY 203 LPSLAIISELSWSALSQIQIASTNNQFESPVVLIINQONQRTITNVDAGVVTSNIAL 262
DB 181 LPSLAIISELSWSALSQIQIASTNNQFESPVVLIINQONQRTITNVDAGVVTSNIAL 240
QY 263 LNRNNMAAMDDVPMTOGFCGGSVAL 289
DB 241 LNRNNMAAMDDVPMTOGFCGGSVAL 267

RESULT 8
US-08-485-286-74
Sequence 74, Application US/08485286
Patent No. 5646026
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B

TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-74

Query Match 92.8%; Score 1328; DB 1; Length 267;
Best Local Similarity 99.6%; Pred. No. 2,4e-128;
Matches 266; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 GVVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPGSGORYALIHITNVADET 82
DB 1 GDVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPGSGORYALIHITNVADET 60

QY 83 ISVAIDVTNVIYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPSGNERLQTAAG 142
DB 61 ISVAIDVTNVIYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPSGNERLQTAAG 120

QY 143 KIRENIPGLPALDSAITTLFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDTFL 202
DB 121 KIRENIPGLPALDSAITTLFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDTFL 180

QY 203 LPSIAIISLNSWSALSQIQIASTNNGQFESPVVLINQONRVITTNVAGVTSINALL 262
DB 181 LPSIAIISLNSWSALSQIQIASTNNGQFESPVVLINQONRVITTNVAGVTSINALL 240

QY 263 LNRNMMAMDDVPMTQSGCGSYAL 289
DB 241 LNRNMMAMDDVPMTQSGCGSYAI 267

RESULT 9
US-08-488-113B-6
Sequence 6, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-113B-6

Query Match 84.5%; Score 1209; DB 1; Length 247;
Best Local Similarity 99.2%; Pred. No. 3.8e-116;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPGSGORYALIHITNVADET 83
DB 1 DVSFRLSGATSSSYGVFISNLKALPNERKLYDIPILRSSLPGSGORYALIHITNVADET 60

QY 84 SVAIIVTVYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPSGNERLQTAAG 143
DB 61 SVAIIVTVYIMGYRAGDTSYFENEASATEAKYVFKDAMRKVTLPSGNERLQTAAG 120

QY 144 IRENIPGLPALDSAITTLFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDTFL 203
DB 121 IRENIPGLPALDSAITTLFYNNANSAASALMWLIQSTSEARVYFIEQIGKRVDTFL 180

QY 204 PSLAIISLNSWSALSQIQIASTNNGQFESPVVLINQONRVITTNVAGVTSINALL 263
DB 181 PSLAIISLNSWSALSQIQIASTNNGQFESPVVLINQONRVITTNVAGVTSINALL 240

QY 264 LNRNMM 270
DB 241 LNRNMM 247

RESULT 10
US-08-477-484B-6
Sequence 6, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-484B-6

Query Match 84.5%; Score 1209; DB 1; Length 247;
Best Local Similarity 99.2%; Pred. No. 3.8e-116;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSLSGQRYVALIHLTNVADDTI 83
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSLSGQRYVALIHLTNVADDTI 60
QY 84 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVFKDMARKYTLFYSGYERLQTPACK 143
DB 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVFKDMARKYTLFYSGYERLQTPACK 120
QY 144 IRENIPLEG.PALDSATITLFFYVANSASALMWL.IOSTSEAAKYKFEQOIGRVKXFTL 203
DB 121 IRENIPLEG.PALDSATITLFFYVANSASALMWL.IOSTSEAAKYKFEQOIGRVKXFTL 180
QY 204 PSIAIISLENSWALSQKQIQAISTNNGQFESPVVLIINAQORVTITNVDAVGTSTNIAL 263
DB 181 PSIAIISLENSWALSQKQIQAISTNNGQFESPVVLIINAQORVTITNVDAVGTSTNIAL 240
QY 264 LNRNMA 270
DB 241 LNRNMA 247

RESULT 11
US-08-646-360-6
Sequence 6, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA

ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-6

Query Match 84.5%; Score 1209; DB 2; Length 247;
Best Local Similarity 99.2%; Pred. No. 3.8e-116;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSLSGQRYVALIHLTNVADDTI 83
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSLSGQRYVALIHLTNVADDTI 60
QY 84 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVFKDMARKYTLFYSGYERLQTPACK 143
DB 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVFKDMARKYTLFYSGYERLQTPACK 120
QY 144 IRENIPLEG.PALDSATITLFFYVANSASALMWL.IOSTSEAAKYKFEQOIGRVKXFTL 203
DB 121 IRENIPLEG.PALDSATITLFFYVANSASALMWL.IOSTSEAAKYKFEQOIGRVKXFTL 180
QY 204 PSIAIISLENSWALSQKQIQAISTNNGQFESPVVLIINAQORVTITNVDAVGTSTNIAL 263
DB 181 PSIAIISLENSWALSQKQIQAISTNNGQFESPVVLIINAQORVTITNVDAVGTSTNIAL 240
QY 264 LNRNMA 270
DB 241 LNRNMA 247

RESULT 12
US-08-839-765-6
Sequence 6, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-6

Query Match 84.5%; Score 1209; DB 3; Length 247;
Best Local Similarity 99.2%; Pred. No. 3.8e-116;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 83
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
QY 84 SVAIDVTNVIYMGVRAAGTSTYFFNEASATEAKYVFKDMRKVTLPSYGNVERLQTPAAK 143
DB 61 SVAIDVTNVIYMGVRAAGTSTYFFNEASATEAKYVFKDMRKVTLPSYGNVERLQTPAAK 120
QY 144 IRENIPLGPAUDSATTTLPYNNANSAASALMWLTIOSTSEARRYKRIEEOIGRVDTKFL 203
DB 121 IRENIPLGPAUDSATTTLPYNNANSAASALMWLTIOSTSEARRYKRIEEOIGRVDTKFL 180
QY 204 PSIAIISLNSWSALSQKQIASTNNGQEPSPVILINAQORVTITNVAGVTSNIALI 263
DB 181 PSIAIISLNSWSALSQKQIASTNNGQEPSPVILINAQORVTITNVAGVTSNIALI 240
QY 264 IRRNNMA 270
|||||

DB 241 IRRNNMA 247

RESULT 13
US-09-136-389-6
Sequence 6, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-136-389-6

Query Match 84.5%; Score 1209; DB 3; Length 247;
Best Local Similarity 99.2%; Pred. No. 3.8e-116;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 83
DB 1 DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI 60
QY 84 SVAIDVTNVIYMGVRAAGTSTYFFNEASATEAKYVFKDMRKVTLPSYGNVERLQTPAAK 143
|||||

Db 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKDMARKVTLLPYSGYVERLQTPACK 120
QY 144 IRENIPGLPALDSATITLFFYNNANSAALMWLIQSTSEAAKYKFEQOIGKRVDTFL 203
Db 121 IRENIPGLPALDSATITLFFYNNANSAALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180
QY 204 PSIAITSLSNSWALSQKQIQIASTNNQGFESPVLINAOQRYTTTNDAGVTSNIALL 263
Db 181 PSIAITSLSNSWALSQKQIQIASTNNQGFESPVLINAOQRYTTTNDAGVTSNIALL 240
QY 264 LNENMMA 270
Db 241 LNENMMA 247
RESULT 14
US-09-610-838-6
Sequence 6, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70-P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-6
Query Match 84.5%; Score 1209; DB 3; Length 247;
Best Local Similarity 99.2%; Pred. No. 3,8e-116;
Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 24 DVSFRLSGATSSSGYGFISNLRKALPNERKLDIPILRRSLPSSQRYALHILNTYADETI 83
Db 1 DVSFRLSGATSSSGYGFISNLRKALPNERKLDIPILRRSLPSSQRYALHILNTYADETI 60
QY 84 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKDMARKVTLLPYSGYVERLQTPACK 143
Db 61 SVAIDVTNYIMGYRAGDTSYFFNEASATEAKYVKDMARKVTLLPYSGYVERLQTPACK 120
QY 144 IRENIPGLPALDSATITLFFYNNANSAALMWLIQSTSEAAKYKFEQOIGKRVDTFL 203
Db 121 IRENIPGLPALDSATITLFFYNNANSAALMWLIQSTSEAAKYKFEQOIGKRVDTFL 180
QY 204 PSIAITSLSNSWALSQKQIQIASTNNQGFESPVLINAOQRYTTTNDAGVTSNIALL 263
Db 181 PSIAITSLSNSWALSQKQIQIASTNNQGFESPVLINAOQRYTTTNDAGVTSNIALL 240
QY 264 LNENMMA 270
Db 241 LNENMMA 247
RESULT 15
US-09-711-485-6
Sequence 6, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.

REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-711-485-6

Query Match 84.5%; Score 1209; DB 4; Length 247;
Best Local Similarity 99.2%; Pred. No. 3.8e-116;

Matches 245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	24	DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI	83
DB	1	DVSFRLSGATSSSYGVFISNLKRALPNERKLYDIPILRSSLPQSORYALIHILTNVADETI	60
QY	84	SVAIIDVTNYIIMGYRAGDTSYFENBASATEAAKYVFKDAMRKVTLPYSGNVERLQTAAGK	143
DB	61	SVAIIDVTNYIIMGYRAGDTSYFENBASATEAAKYVFKDAMRKVTLPYSGNVERLQTAAGK	120
QY	144	IRENIPILG.PALDSAITTLFYNNANSASALMWLIQSTSEAAKYKFEQOIGKVDKTFI	203
DB	121	IRENIPILG.PALDSAITTLFYNNANSASALMWLIQSTSEAAKYKFEQOIGKVDKTFI	180
QY	204	PSLAITISLENSWSALSQIQIASTNNGQFESPVLINAOQRYTITNVDAGVVTSNIALI	263
DB	181	PSLAITISLENSWSALSQIQIASTNNGQFESPVLINAOQRYTITNVDAGVVTSNIALI	240
QY	264	LNRRNNMA 270	
DB	241	LNRRNNMA 247	

Search completed: April 12, 2005, 15:16:14
Job time : 38.2034 secs